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OM protein - protein search, using sw model

Run on: August 31, 2001, 15:59:56 ; Search time 12.19 Seconds  
(without alignments)  
47.295 Million cell updates/sec

Title: US-09-448-867-1

Perfect score: 137

Sequence: 1 XVSEIQLMHNIGKHLNMXRVWLKKL 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	134	97.8	30	1	US-08-262-495C-5
2	134	97.8	31	1	US-08-262-495C-3
3	134	97.8	31	2	US-08-691-647C-1
4	134	97.8	31	2	US-08-691-647C-6
5	134	97.8	31	3	US-08-904-760B-1
6	134	97.8	31	3	US-08-904-760B-6
7	134	97.8	31	3	US-08-904-760B-14
8	134	97.8	31	3	US-08-904-760B-32
9	134	97.8	34	1	US-07-765-373-1
10	134	97.8	34	1	US-08-033-099-1
11	134	97.8	34	1	US-08-262-495C-1
12	134	97.8	34	1	US-07-915-247A-1
13	134	97.8	34	1	US-08-443-863-1
14	134	97.8	34	1	US-08-448-070-1
15	134	97.8	34	1	US-08-488-105-7
16	134	97.8	34	1	US-08-468-275-6
17	134	97.8	34	1	US-08-449-500-1
18	134	97.8	34	1	US-08-449-317A-1
19	134	97.8	34	2	US-08-142-551B-2
20	134	97.8	34	2	US-08-477-022-1
21	134	97.8	34	2	US-08-449-447-1
22	134	97.8	34	2	US-08-835-231-13
23	134	97.8	34	2	US-08-184-328-1
24	134	97.8	34	2	US-08-411-726-2
25	134	97.8	34	2	US-08-691-647C-5
26	134	97.8	34	2	US-08-521-097-1
27	134	97.8	34	3	US-09-044-536A-1

28	134	97.8	34	3	US-08-904-760B-22	Sequence 22, Appl
29	134	97.8	34	4	US-08-903-497A-1	Sequence 1, Appl
30	134	97.8	34	5	PCT-US95-15800-22	Sequence 22, Appl
31	134	97.8	35	1	US-08-256-363-3	Sequence 3, Appl
32	134	97.8	36	1	US-08-112-024-2	Sequence 2, Appl
33	134	97.8	36	1	US-08-256-363-4	Sequence 4, Appl
34	134	97.8	37	1	US-08-440-117-1	Sequence 1, Appl
35	134	97.8	37	4	US-09-068-738A-16	Sequence 16, Appl
36	134	97.8	38	1	US-08-112-024-1	Sequence 1, Appl
37	134	97.8	38	1	US-08-232-849-1	Sequence 1, Appl
38	134	97.8	38	2	US-08-625-586-1	Sequence 1, Appl
39	134	97.8	38	3	US-09-128-401-1	Sequence 1, Appl
40	134	97.8	84	1	US-07-707-114-1	Sequence 1, Appl
41	134	97.8	84	1	US-07-773-098-2	Sequence 2, Appl
42	134	97.8	84	1	US-07-863-014-2	Sequence 2, Appl
43	134	97.8	84	1	US-08-332-453-2	Sequence 2, Appl
44	134	97.8	84	1	US-08-689-190-2	Sequence 2, Appl
45	134	97.8	84	2	US-08-142-551B-1	Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-08-262-495C-5  
; Sequence 5, Application US/08262495C  
; Patent No. 5556940  
; GENERAL INFORMATION:  
; APPLICANT: WILLICK, Gordon E.  
; APPLICANT: WHITFIELD, James F.  
; APPLICANT: SUREWICZ, Witold  
; APPLICANT: SUNG, Wing L.  
; APPLICANT: NEUGENBAUER, Witold  
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES  
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Kirby, Eades, Gale, Baker  
; STREET: 112 Kent Street, Suite 770,  
; CITY: Ottawa  
; COUNTRY: Canada  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/262.495C  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: EADES, No. 5556940ris M.  
; REGISTRATION NUMBER: 5,263  
; REFERENCE/DOCKET NUMBER: 36210  
; TELEPHONE: (613)-237-6900  
; TELEFAX: (613)-237-0045  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-262-495C-5

Query Match 97.8%; Score 134; DB 1; Length 30;  
Best Local Similarity 96.3%; Pred. No. 7.6e-13;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMXRVWELRKKL 28  
|||||  
Db 2 VSEIQLMHNLGKHLNSMERVWELRKKL 28

RESULT 2  
US-08-262-495C-3  
; Sequence 3, Application US/08262495C  
; Patent No. 5556940  
; GENERAL INFORMATION:  
; APPLICANT: WILLICK, Gordon E.  
; APPLICANT: WHITFIELD, James F.  
; APPLICANT: SUREWICZ, Witold  
; APPLICANT: SUNG, Wing L.  
; APPLICANT: NEUGEBAUER, Witold  
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES  
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kirby, Eades, Gale, Baker  
; STREET: 112 Kent Street, Suite 770,  
; CITY: Ottawa  
; COUNTRY: Canada  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/262,495C  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: EADES, No. 5556940rls M.  
; REGISTRATION NUMBER: 5,263  
; REFERENCE/DOCKET NUMBER: 36210  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (613)-237-6900  
; TELEFAX: (613)-237-0045  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 31 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-262-495C-3

Query Match 97.8%; Score 134; DB 1; Length 31;  
Best Local Similarity 96.3%; Pred. No. 7.9e-13;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMXRVWELRKKL 28  
|||||  
Db 2 VSEIQLMHNLGKHLNSMERVWELRKKL 28

RESULT 3  
US-08-691-647C-1  
; Sequence 1, Application US/08691647C  
; Patent No. 5955425  
; GENERAL INFORMATION:  
; APPLICANT: Barbier, Jean-Rene  
; APPLICANT: Morley, Paul  
; APPLICANT: Neugebauer, Witold  
; APPLICANT: Ross, Virginia  
; APPLICANT: WHITFIELD, James  
; APPLICANT: Willick, Gordon E.

; TITLE OF INVENTION: CYCLIC PARATHYROID HORMONE ANALOGUES  
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE, P.C.  
; STREET: 1100 New York Avenue, 8th Floor  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/691,647C  
; FILING DATE: August 2, 1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Crawford, Arthur R.  
; REGISTRATION NUMBER: 25,327  
; REFERENCE/DOCKET NUMBER: 1339-5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4005  
; TELEFAX: (703) 816-4100  
; TELEX: N/A  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 31 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-691-647C-1

Query Match 97.8%; Score 134; DB 2; Length 31;  
Best Local Similarity 96.3%; Pred. No. 7.9e-13;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMXRVWELRKKL 28  
|||||  
Db 2 VSEIQLMHNLGKHLNSMERVWELRKKL 28

RESULT 4  
US-08-691-647C-6  
; Sequence 6, Application US/08691647C  
; Patent No. 5955425  
; GENERAL INFORMATION:  
; APPLICANT: Barbier, Jean-Rene  
; APPLICANT: Morley, Paul  
; APPLICANT: Neugebauer, Witold  
; APPLICANT: Ross, Virginia  
; APPLICANT: WHITFIELD, James  
; APPLICANT: Willick, Gordon E.  
; TITLE OF INVENTION: CYCLIC PARATHYROID HORMONE ANALOGUES  
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE, P.C.  
; STREET: 1100 New York Avenue, 8th Floor  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/691,647C

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1: INFORMATION FOR SEQ ID NO: 1:
2:
3: SEQUENCE CHARACTERISTICS:
4:     LENGTH: 31 amino acids
5:     TYPE: amino acid
6:     STRANDEDNESS:
7:     TOPOLOGY: linear

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; FEATURE:  
 ; OTHER INFORMATION: cyclo Lys27-Asp30, and this sequence  
 ; OTHER INFORMATION: has an amino group c-terminus (NH2).  
 US-08-904-760B-6

QY 2 VSEIQLMHNLGKHLNSMXRVEWLRKKL 28  
 |||||  
 db 2 VSEIOLMHNLGKHLNSMERVEWLRKKL 28  
 |||||

RESULT 7  
US-08-904-760B-14  
; Sequence 14, Application US/08904760B  
; Patent No. 6110892  
; GENERAL INFORMATION:  
; APPLICANT: Jean-Rene, Barbier  
; APPLICANT: Neugebauer, Witold  
; APPLICANT: Ross, Virginia  
; APPLICANT: Whitfield, James  
; APPLICANT: Willick, Gordon E.  
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE  
; TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHVE P.C.  
; STREET: 1100 No. 6110892th Glebe Rd. 8th floor  
; CITY: Arlington  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201-4741  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/904,760B  
; FILING DATE: 01-AUG-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/691,647  
; FILING DATE: 02-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Crawford, Arthur R.  
; REGISTRATION NUMBER: 25,327  
; REFERENCE/DOCKET NUMBER: 1339-6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4000  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 31 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: circular  
; FEATURE:  
; OTHER INFORMATION: cyclo Glu22-Lys26, and this sequence  
; OTHER INFORMATION: has an amino group c-terminus (NH2).  
US-08-904-760B-14

Query Match 97.8%; Score 134; DB 3; Length 31;  
Best Local Similarity 96.3%; Pred. No. 7.9e-13;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 VSEIQLMHNLGKHLNSMXRVEWLRRKL 28  
|||||  
DB 2 VSEIQLMHNLGKHLNSMERVEWLRRKL 28  
|||||  
  
RESULT 8  
US-08-904-760B-32  
; Sequence 32, Application US/08904760B  
; Patent No. 6110892  
; GENERAL INFORMATION:  
; APPLICANT: Jean-Rene, Barbier  
; APPLICANT: Neugebauer, Witold  
; APPLICANT: Ross, Virginia  
; APPLICANT: Whitfield, James  
; APPLICANT: Willick, Gordon E.  
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE

; TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHVE P.C.  
; STREET: 1100 No. 6110892th Glebe Rd. 8th floor  
; CITY: Arlington  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201-4741  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/904,760B  
; FILING DATE: 01-AUG-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/691,647  
; FILING DATE: 02-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Crawford, Arthur R.  
; REGISTRATION NUMBER: 25,327  
; REFERENCE/DOCKET NUMBER: 1339-6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4000  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 31 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; OTHER INFORMATION: This sequence has an amino group  
; OTHER INFORMATION: c-terminus (NH2).  
US-08-904-760B-32  
  
Query Match 97.8%; Score 134; DB 3; Length 31;  
Best Local Similarity 96.3%; Pred. No. 7.9e-13;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 VSEIQLMHNLGKHLNSMXRVEWLRRKL 28  
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DB 2 VSEIQLMHNLGKHLNSMERVEWLRRKL 28  
|||||  
  
RESULT 9  
US-07-765-373-1  
; Sequence 1, Application US/07765373  
; Patent No. 5393869  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, Shizue  
; APPLICANT: FUKUDA, Tsunehiko  
; APPLICANT: KAWASE, Masahiro  
; APPLICANT: YAMAZAKI, Iwao  
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
; ADDRESSEE: CUSHMAN  
; STREET: 130 Water Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/765,373  
FILING DATE: 19910925  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAMS, Gregory D.  
REGISTRATION NUMBER: 30901  
REFERENCE/DOCKET NUMBER: 41289  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
-TELEX: 20091 STRE UR  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: N-terminal  
US-07-765-373-1

Query Match 97.8%; Score 134; DB 1; Length 34;  
Best Local Similarity 96.3%; Pred. No. 8.7e-13;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNGLKHLNSMRVWLRLKKL 28  
|||||  
Db 2 VSEIQLMHNGLKHLNSMRVWLRLKKL 28

RESULT 10  
US-08-033-099-1  
Sequence 1, Application US/08033099  
Patent No. 5434246  
GENERAL INFORMATION:  
APPLICANT: FUKUDA, Tsunehiko  
APPLICANT: NAKAGAWA, Shizue  
APPLICANT: TAKETOMI, Shigehisa  
TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
ADDRESSEE: CUSHMAN  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/033,099  
FILING DATE: 19930316  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: WILLIAMS, Gregory D.  
REGISTRATION NUMBER: 30901  
REFERENCE/DOCKET NUMBER: 42528  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
-TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein

FRAGMENT TYPE: N-terminal  
US-08-033-099-1

Query Match 97.8%; Score 134; DB 1; Length 34;  
Best Local Similarity 96.3%; Pred. No. 8.7e-13;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNGLKHLNSMRVWLRLKKL 28  
|||||  
Db 2 VSEIQLMHNGLKHLNSMRVWLRLKKL 28

RESULT 11  
US-08-262-495C-1  
Sequence 1, Application US/08262495C  
Patent No. 5556940  
GENERAL INFORMATION:  
APPLICANT: WILLICK, Gordon E.  
APPLICANT: WHITEFIELD, James F.  
APPLICANT: SUREWICZ, Witold  
APPLICANT: SUNG, Wing L.  
APPLICANT: NEUGENBAUER, Witold  
TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES  
TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kirby, Eades, Gale, Baker  
STREET: 112 Kent Street, Suite 770,  
CITY: Ottawa  
COUNTRY: Canada  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/262,495C  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: EADES, No. 5556940ris M.  
REGISTRATION NUMBER: 5,263  
REFERENCE/DOCKET NUMBER: 36210  
TELEPHONE: (613)-237-6900  
TELEFAX: (613)-237-0045  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-262-495C-1

Query Match 97.8%; Score 134; DB 1; Length 34;  
Best Local Similarity 96.3%; Pred. No. 8.7e-13;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNGLKHLNSMRVWLRLKKL 28  
|||||  
Db 2 VSEIQLMHNGLKHLNSMRVWLRLKKL 28

RESULT 12  
US-07-915-247A-1  
Sequence 1, Application US/07915247A  
Patent No. 5589452

```

; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/915,247A
; FILING DATE: 19920714
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; US-07-915-247A-1

Query Match 97.8%; Score 134; DB 1; Length 34;
Best Local Similarity 96.3%; Pred. No. 8.7e-13;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQLMHNGLKHLNSMXRVEWLRRKL 28
| | | | | | | | | | | | | | | | | |
Db 2 VSEIQLMHNGLKHLNSMERVEWLRRKL 28

RESULT 13
US-08-443-863-1
; Sequence 1, Application US/08443863
; Patent No. 5693616
; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA

; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,070
; FILING DATE: 14-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; US-08-443-863-1

Query Match 97.8%; Score 134; DB 1; Length 34;
Best Local Similarity 96.3%; Pred. No. 8.7e-13;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQLMHNGLKHLNSMXRVEWLRRKL 28
| | | | | | | | | | | | | | | | | |
Db 2 VSEIQLMHNGLKHLNSMERVEWLRRKL 28

RESULT 14
US-08-448-070-1
; Sequence 1, Application US/08448070
; Patent No. 5695955
; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,070
; FILING DATE: 14-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; US-08-443-863-1
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TELEFAX: 415-496-3529  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 34 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 FRAGMENT TYPE: N-terminal  
 US-08-448-070-1

Query Match 97.8%; Score 134; DB 1; Length 34;  
 Best Local Similarity 96.3%; Pred. No. 8.7e-13;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMXRVWLRLKKL 28  
 Db 2 VSEIQLMHNLGKHLNSMXRVWLRLKKL 28

Search completed: August 31, 2001, 16:00:17  
 Job time: 21 sec

TELEFAX: 415-496-3529  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 34 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 FRAGMENT TYPE: N-terminal  
 US-08-448-070-1

Query Match 97.8%; Score 134; DB 1; Length 34;  
 Best Local Similarity 96.3%; Pred. No. 8.7e-13;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMXRVWLRLKKL 28  
 Db 2 VSEIQLMHNLGKHLNSMXRVWLRLKKL 28

Search completed: August 31, 2001, 16:00:17  
 Job time: 21 sec

RESULT 15  
 US-08-488-105-7  
 Sequence 7, Application US/08488105  
 Patent No. 5717062  
 GENERAL INFORMATION:  
 APPLICANT: Chorev, Michael  
 APPLICANT: Rosenblatt, Michael  
 TITLE OF INVENTION: CYCLIC ANALOGS OF PTH AND PTHR  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/488,105  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Tsao, Y. Rocky  
 REGISTRATION NUMBER: 34,053  
 REFERENCE/DOCKET NUMBER: 00537/112001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 34 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 OTHER INFORMATION: The side chains of Lys at  
 OTHER INFORMATION: position 26 and Asp at position 30 are linked by an amide bond  
 OTHER INFORMATION: and this sequence has an amide C-terminus (i.e., CONH2), rather  
 OTHER INFORMATION: than a carboxy C-terminus (i.e., COOH).  
 US-08-488-105-7

Query Match 97.8%; Score 134; DB 1; Length 34;  
 Best Local Similarity 96.3%; Pred. No. 8.7e-13;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 31, 2001, 15:59:56 ; Search time 18.06 Seconds  
(without alignments)  
93.991 Million cell updates/sec

Title: US-09-448-867-1

Perfect score: 137

Sequence: 1 XVSFIQLMNLGKHLNMXRVLEWLKRL 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
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6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
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15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	135	98.5	36	15	AA1919-hPTH(1-36)
2	135	98.5	38	15	AA1919-hPTH(1-38)
3	135	98.5	38	15	AA1919-hPTH(1-38)
4	134	97.8	28	17	AA1919-hPTH(1-38)
5	134	97.8	28	21	AA1919-hPTH(1-38)
6	134	97.8	28	21	AA1919-hPTH(1-38)
7	134	97.8	28	21	AA1919-hPTH(1-38)
8	134	97.8	28	21	AA1919-hPTH(1-38)
9	134	97.8	28	21	AA1919-hPTH(1-38)
10	134	97.8	28	21	AA1919-hPTH(1-38)
11	134	97.8	28	21	AA1919-hPTH(1-38)

12	134	97.8	29	12	AA11731	Adenine-rich pTH-(
13	134	97.8	29	17	AA18836	Human parathyroid
14	134	97.8	30	17	AA18832	Human parathyroid
15	134	97.8	31	19	AA142051	Human parathyroid
16	134	97.8	31	19	AA142051	Human parathyroid
17	134	97.8	31	20	AA102578	N-terminal 31 resi
18	134	97.8	33	21	AA198012	Human amino-termin
19	134	97.8	33	21	AA198015	Human amino-termin
20	134	97.8	33	21	AA198018	Human amino-termin
21	134	97.8	34	4	AA130022	Human parathyroid-(
22	134	97.8	34	6	AA150377	[Met(O)18,18]hPTH-(
23	134	97.8	34	7	AA160031	Sequence of the fi
24	134	97.8	34	11	AA107919	Human parathyroid
25	134	97.8	34	11	AA107922	Human parathyroid
26	134	97.8	34	13	AA122283	Parathyroid hormone
27	134	97.8	34	14	AA141549	[D-Ser3]hPTH (1-34
28	134	97.8	34	14	AA141570	[Gln25]hPTH (1-34)
29	134	97.8	34	15	AA158291	[Lys(For)26, Lys(F
30	134	97.8	34	15	AA158228	[D-Asp30]-hPTH(1-3
31	134	97.8	34	15	AA158232	[Lys33]-hPTH(1-34)
32	134	97.8	34	15	AA158181	[Thr33, Ala34]-hPT
33	134	97.8	34	15	AA158016	N-alpha-Isopropyl-
34	134	97.8	34	15	AA158017	[Lys(N-epsilon)-Iso
35	134	97.8	34	15	AA155724	Parathormone N-ter
36	134	97.8	34	16	AA174521	Human parathyroid
37	134	97.8	34	17	AA199449	Human parathyroid
38	134	97.8	34	17	AA199978	Human parathyroid
39	134	97.8	34	17	AA198951	Target peptide (PT
40	134	97.8	34	17	AA198966	PTH(1-34). Not sp
41	134	97.8	34	17	AA188835	Human parathyroid
42	134	97.8	34	18	AA124273	Wild type parathyr
43	134	97.8	34	18	AA119994	Cyclised human par
44	134	97.8	34	18	AA120000	Cyclised human par
45	134	97.8	34	19	AA167283	Parathyroid hormone

#### ALIGNMENTS

RESULT 1

AA1919-hPTH(1-36) standard; peptide; 36 AA.

AC AA1919-hPTH(1-36)

DT 20-SEP-1994 (first entry)

DE [Ala19]-hPTH(1-36)-NH2.

Human parathyroid hormone; hPTH; variant; analogue;

calcium; depletion; fixation; resorption; osteoporosis;

hypoparathyroidism.

OS Synthetic.

Key Location/Qualifiers

Modified-site 36

/note= "in amide form"

GB2269176-A.

02-FEB-1994.

12-JUL-1993;

93GB-0014384.

15-JUL-1992;

92GB-0015009.

18-DEC-1992;

92GB-0026415.

23-DEC-1992;

92GB-0026859.

23-DEC-1992;

92GB-0026861.

28-JAN-1993;

93GB-0001691.

28-JAN-1993;

93GB-0001692.

14-APR-1993;

93GB-0007673.

19-APR-1993;

93GB-0008033.

XX (SANO ) SANDOZ LTD.  
 PA (BAUE/) BAUER W.  
 PA (SANO ) SANDOZ PATENT GMBH.  
 PA (SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.  
 XX  
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;  
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;  
 PI Waelchli R, Rainer A;  
 XX  
 DR WPI; 1994-018352/03.  
 XX  
 XX New active para-thyroid hormone variants - used for treating or  
 PT preventing osteoporosis etc.  
 XX  
 PS Example 212; Page 44; 92pp; English.  
 XX  
 CC This peptide is an example of a highly generic formula covering  
 CC parathyroid hormone variants useful for treating or preventing bone  
 CC conditions associated with calcium depletion/resorption, in cases  
 CC where calcium fixation is required (esp. osteoporosis) or to treat  
 CC hypoparathyroidism.  
 XX  
 SQ Sequence 36 AA;  
 XX  
 XX Query Match 98.5%; Score 135; DB 15; Length 36;  
 XX Best Local Similarity 96.3%; Pred. No. 3.5e-13;  
 XX Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 VSEIOLMHNIGKHLNSMXRVEWLKKL 28  
 Db 2 vseiqimhngkhlnsmarvewlrkkl 28  
 OK  
 RESULT 2  
 AAR58123  
 ID AAR58123 standard; peptide; 38 AA.  
 XX  
 AC AAR58123;  
 XX  
 DT 20-SEP-1994 (first entry)  
 XX  
 DE [Ser19]-hPTH(1-38)-OH.  
 XX  
 KW Human parathyroid hormone; hPTH; variant; analogue;  
 KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;  
 KW hypoparathyroidism.  
 XX  
 OS Synthetic.  
 XX  
 PN GB2269176-A.  
 XX  
 PD 02-FEB-1994.  
 XX  
 PF 12-JUL-1993; 93GB-0014384.  
 XX  
 PR 15-JUL-1992; 92GB-0015009.  
 PR 18-DEC-1992; 92GB-0026415.  
 PR 23-DEC-1992; 92GB-0026859.  
 PR 23-DEC-1992; 92GB-0026861.  
 PR 28-JAN-1993; 93GB-0001691.  
 PR 28-JAN-1993; 93GB-0001692.  
 PR 14-APR-1993; 93GB-0007673.  
 PR 19-APR-1993; 93GB-0008033.  
 XX  
 PA (SANO ) SANDOZ LTD.  
 PA (BAUE/) BAUER W.  
 PA (SANO ) SANDOZ PATENT GMBH.  
 PA (SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.  
 XX  
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;  
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;  
 XX

PI Waelchli R, Rainer A;  
 XX  
 DR WPI; 1994-018352/03.  
 XX  
 XX New active para-thyroid hormone variants - used for treating or  
 PT preventing osteoporosis etc.  
 XX  
 PS Example 120; Page 39; 92pp; English.  
 XX  
 CC This peptide is an example of a highly generic formula covering  
 CC parathyroid hormone variants useful for treating or preventing bone  
 CC conditions associated with calcium depletion/resorption, in cases  
 CC where calcium fixation is required (esp. osteoporosis) or to treat  
 CC hypoparathyroidism.  
 XX  
 SQ Sequence 38 AA;  
 XX  
 XX Query Match 98.5%; Score 135; DB 15; Length 38;  
 XX Best Local Similarity 96.3%; Pred. No. 3.7e-13;  
 XX Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 VSEIOLMHNIGKHLNSMXRVEWLKKL 28  
 Db 2 vseiqimhngkhlnsmarvewlrkkl 28  
 RESULT 3  
 AAR58126  
 ID AAR58126 standard; peptide; 38 AA.  
 XX  
 AC AAR58126;  
 XX  
 DT 20-SEP-1994 (first entry)  
 XX  
 DE [Ala19]-hPTH(1-38)-OH.  
 XX  
 KW Human parathyroid hormone; hPTH; variant; analogue;  
 KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;  
 KW hypoparathyroidism.  
 XX  
 OS Synthetic.  
 XX  
 PN GB2269176-A.  
 XX  
 PD 02-FEB-1994.  
 XX  
 PF 12-JUL-1993; 93GB-0014384.  
 XX  
 PR 15-JUL-1992; 92GB-0015009.  
 PR 18-DEC-1992; 92GB-0026415.  
 PR 23-DEC-1992; 92GB-0026859.  
 PR 23-DEC-1992; 92GB-0026861.  
 PR 28-JAN-1993; 93GB-0001691.  
 PR 28-JAN-1993; 93GB-0001692.  
 PR 14-APR-1993; 93GB-0007673.  
 PR 19-APR-1993; 93GB-0008033.  
 XX  
 PA (SANO ) SANDOZ LTD.  
 PA (BAUE/) BAUER W.  
 PA (SANO ) SANDOZ PATENT GMBH.  
 PA (SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.  
 XX  
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;  
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;  
 PI Waelchli R, Rainer A;  
 XX  
 DR WPI; 1994-018352/03.  
 XX  
 XX New active para-thyroid hormone variants - used for treating or  
 PT preventing osteoporosis etc.  
 XX  
 PS Example 123; Page 39; 92pp; English.

Query Match 97.8%; Score 134; DB 17; Length 28;  
Best Local Similarity 96.3%; Pred. No. 3.7e-13;  
Matches 26; Conservative 0; Mismatches 1; Indels

Query Match 97.8%; Score 134; DB 21; Length 28;  
Best Local Similarity 100.0%; Pred. No. 3.7e-13;  
Matches 27; Conservative 0; Mismatches 0; Indels

Query Match	97.8%	Score 134;	DB 21;	Length 28;
Best Local Similarity	100.0%;	Pred. No. 3.7e-13;		
Matches 27;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 2 VSEIQLMHNGLGKHLNSMXRVLEWLRKKL 28  
 DB 2 vseiqlmhnlghlnsmrxrvlewlrkkl 28

RESULT 6  
 AAY98042  
 ID AAY98042 standard; peptide; 28 AA.  
 AC AAY98042;  
 XX  
 DT 04-SEP-2000 (first entry)  
 DE Human parathyroid hormone peptide # 2.  
 XX Human; parathyroid hormone; signal transduction; osteoporosis;  
 KW osteopaenia; hypoparathyroidism; fracture repair; hypercalcaemia;  
 KW breast cancer; lung cancer; prostate cancer; multiple myeloma;  
 KW hypernephroma; head and neck epidermoid cancer; oesophagus cancer;  
 KW osteopathic; PTH.  
 XX Homo sapiens.  
 OS  
 XX WO200031266-A1.  
 PN  
 XX 02-JUN-2000.  
 PD  
 XX 24-NOV-1999; 99WO-US27863.  
 PF  
 XX 25-NOV-1998; 98US-0109938.  
 PR  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA  
 XX Brighthurst FR, Takasu H, Gardella TJ, Potts JT;  
 PI  
 XX WPI; 2000-400076/34.  
 DR  
 XX Novel biologically active peptide comprising a parathyroid hormone  
 PT peptide derivative, useful for treating osteoporosis -  
 XX  
 PS Claim 5; Page 67; 75pp; English.

Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous cells, initiating signal transduction. It has been identified that the carboxyl terminal of PTH is important for PTH receptor binding, while the amino terminal is important for signal transduction. Various PTH peptides were produced with amino- and carboxy terminal modifications which had varying PTH receptor activation properties and therefore downstream signalling. Aberrant PTH activity has been implicated in a number of disorders: osteoporosis, osteopaenia, hypoparathyroidism and hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma and a variety of cancers: breast, lung and prostate carcinoma, multiple myeloma and epidermoid cancers of the head, neck and oesophagus. The present sequence is a PTH peptide, with a Gly residue at position 1 and an Arg residue at position 19. The Gly residue reduces downstream signalling via phospholipase C (PLC), whereas the Arg residue restores PLC signalling and ligand binding. The present peptide may therefore be used as a PTH receptor agonist for the treatment of the above mentioned disorders. In addition, the present sequence would be suitable for fracture repair.

QY 2 VSEIQLMHNGLGKHLNSMXRVLEWLRKKL 28  
 DB 2 vseiqlmhnlghlnsmrxrvlewlrkkl 28

Query Match 97.8%; Score 134; DB 21; Length 28;  
 Best Local Similarity 96.3%; Pred. No. 3.7e-13;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 7  
 AAY98044  
 ID AAY98044 standard; peptide; 28 AA.  
 AC AAY98044;  
 XX  
 DT 04-SEP-2000 (first entry)  
 DE Human parathyroid hormone peptide # 4.  
 XX Human; parathyroid hormone; signal transduction; osteoporosis;  
 KW osteopaenia; hypoparathyroidism; fracture repair; hypercalcaemia;  
 KW breast cancer; lung cancer; prostate cancer; multiple myeloma;  
 KW hypernephroma; head and neck epidermoid cancer; oesophagus cancer;  
 KW osteopathic; PTH.  
 XX Homo sapiens.  
 OS  
 XX WO200031266-A1.  
 PN  
 XX 02-JUN-2000.  
 PD  
 XX 24-NOV-1999; 99WO-US27863.  
 PF  
 XX 25-NOV-1998; 98US-0109938.  
 PR  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA  
 XX Brighthurst FR, Takasu H, Gardella TJ, Potts JT;  
 PI  
 XX WPI; 2000-400076/34.  
 DR  
 XX Novel biologically active peptide comprising a parathyroid hormone  
 PT peptide derivative, useful for treating osteoporosis -  
 XX  
 PS Claim 6; Page 68; 75pp; English.

Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous cells, initiating signal transduction. It has been identified that the carboxyl terminal of PTH is important for PTH receptor binding, while the amino terminal is important for signal transduction. Various PTH peptides were produced with amino- and carboxy terminal modifications which had varying PTH receptor activation properties and therefore downstream signalling. Aberrant PTH activity has been implicated in a number of disorders: osteoporosis, osteopaenia, hypoparathyroidism and hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma and a variety of cancers: breast, lung and prostate carcinoma, multiple myeloma and epidermoid cancers of the head, neck and oesophagus. The present sequence is a PTH peptide, with an Ala residue at position 1 and an Arg residue at position 19. The Ala and Arg residues both improve downstream signalling via phospholipase C (PLC) and ligand binding. The present peptide may therefore be used as a PTH receptor agonist for the treatment of the above mentioned disorders. In addition, the present sequence would be suitable for fracture repair.

QY 2 VSEIQLMHNGLGKHLNSMXRVLEWLRKKL 28  
 DB 2 vseiqlmhnlghlnsmrxrvlewlrkkl 28

Query Match 97.8%; Score 134; DB 21; Length 28;  
 Best Local Similarity 96.3%; Pred. No. 3.7e-13;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 8  
 AAY98046  
 ID AAY98046 standard; peptide; 28 AA.  
 AC AAY98046;  
 XX

DT 04-SEP-2000 (first entry)  
 DE Human parathyroid hormone peptide # 6.  
 XX  
 KW Human; parathyroid hormone; signal transduction; osteoporosis;  
 KW osteopaenia; hypoparathyroidism; fracture repair; hypercalcaemia;  
 KW breast cancer; lung cancer; prostate cancer; multiple myeloma;  
 KW hypernephroma; head and neck epidermoid cancer; oesophagus cancer;  
 KW osteopathic; PTH.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200031266-A1.  
 PN  
 XX 02-JUN-2000.  
 PD  
 XX 24-NOV-1999; 99WO-US27863.  
 XX  
 XX 25-NOV-1998; 98US-0109938.  
 PF  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PR  
 XX Bringhurst FR, Takasu H, Gardella TJ, Potts JT;  
 XX WPI; 2000-400076/34.  
 XX  
 XX Novel biologically active peptide comprising a parathyroid hormone  
 PT peptide derivative, useful for treating osteoporosis -  
 PT  
 XX Claim 9; Page 68; 75pp; English.  
 PS  
 XX Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous  
 CC cells, initiating signal transduction. It has been identified that the  
 CC carboxyl terminal of PTH is important for PTH receptor binding, while the  
 CC amino terminal is important for signal transduction. Various PTH peptides  
 CC were produced with amino- and carboxy terminal modifications which had  
 CC varying PTH receptor activation properties and therefore downstream  
 CC signalling. Aberrant PTH activity has been implicated in a number of  
 CC disorders: osteoporosis, osteopaenia, hypoparathyroidism and  
 CC hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma  
 CC and a variety of cancers: breast, lung and prostate carcinoma, multiple  
 CC myeloma and epidermoid cancers of the head, neck and oesophagus. The  
 CC present sequence is a PTH peptide, with a Ser residue at position 1 and  
 CC an Arg residue at position 19. The Ser and Arg residues both improve  
 CC downstream signalling via phospholipase C (PLC) and ligand binding. The  
 CC present peptide may therefore be used as a PTH receptor agonist for the  
 CC treatment of the above mentioned disorders. In addition, the present  
 CC sequence would be suitable for fracture repair.  
 XX  
 SQ Sequence 28 AA;  
 Query Match 97.8%; Score 134; DB 21; Length 28;  
 Best Local Similarity 96.3%; Pred. NO. 3.7e-13;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 2 VSEIQLMHNIGKHLNSMXRVLEWLRKKL 28  
 DB 2 VSEIQLMHNIGKHLNSMXRVLEWLRKKL 28  
 RESULT 9  
 AAY98048  
 ID AAY98048 standard; peptide; 28 AA.  
 XX  
 AC AAY98048;  
 XX  
 XX 04-SEP-2000 (first entry)  
 XX Human parathyroid hormone peptide # 8.  
 DE- Human; parathyroid hormone; signal transduction; osteoporosis;  
 KW osteopaenia; hypoparathyroidism; fracture repair; hypercalcaemia;  
 KW

KW breast cancer; lung cancer; prostate cancer; multiple myeloma;  
 KW hypernephroma; head and neck epidermoid cancer; oesophagus cancer;  
 KW osteopathic; PTH.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200031266-A1.  
 PN  
 XX 02-JUN-2000.  
 PD  
 XX 24-NOV-1999; 99WO-US27863.  
 XX  
 XX 25-NOV-1998; 98US-0109938.  
 PF  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PR  
 XX Bringhurst FR, Takasu H, Gardella TJ, Potts JT;  
 XX WPI; 2000-400076/34.  
 XX  
 XX Novel biologically active peptide comprising a parathyroid hormone  
 PT peptide derivative, useful for treating osteoporosis -  
 PT  
 XX Claim 8; Page 69; 75pp; English.  
 PS  
 XX Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous  
 CC cells, initiating signal transduction. It has been identified that the  
 CC carboxyl terminal of PTH is important for PTH receptor binding, while the  
 CC amino terminal is important for signal transduction. Various PTH peptides  
 CC were produced with amino- and carboxy terminal modifications which had  
 CC varying PTH receptor activation properties and therefore downstream  
 CC signalling. Aberrant PTH activity has been implicated in a number of  
 CC disorders: osteoporosis, osteopaenia, hypoparathyroidism and  
 CC hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma  
 CC and a variety of cancers: breast, lung and prostate carcinoma, multiple  
 CC myeloma and epidermoid cancers of the head, neck and oesophagus. The  
 CC present sequence is a PTH peptide, with an Ala residue at position 1 and  
 CC a Glu residue at position 19. The Ala residue improves downstream  
 CC signalling via phospholipase C (PLC), whereas the Glu residue reduces PLC  
 CC signalling and ligand binding. PTH peptides with a Arg residue at  
 CC position 19 have improved PLC signalling and ligand binding and so may be  
 CC used as a PTH receptor agonist for the treatment of the above mentioned  
 CC disorders and fracture repair.  
 XX  
 SQ Sequence 28 AA;  
 Query Match 97.8%; Score 134; DB 21; Length 28;  
 Best Local Similarity 96.3%; Pred. NO. 3.7e-13;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 2 VSEIQLMHNIGKHLNSMXRVLEWLRKKL 28  
 DB 2 VSEIQLMHNIGKHLNSMXRVLEWLRKKL 28  
 RESULT 10  
 AAY98050  
 ID AAY98050 standard; peptide; 28 AA.  
 XX  
 AC AAY98050;  
 XX  
 XX 04-SEP-2000 (first entry)  
 XX Human parathyroid hormone peptide # 10.  
 DE Human; parathyroid hormone; signal transduction; osteoporosis;  
 KW osteopaenia; hypoparathyroidism; fracture repair; hypercalcaemia;  
 KW breast cancer; lung cancer; prostate cancer; multiple myeloma;  
 KW hypernephroma; head and neck epidermoid cancer; oesophagus cancer;  
 KW osteopathic; PTH.  
 XX  
 XX Homo sapiens.  
 OS

XX WO200031266-A1.  
PN XX  
XX 02-JUN-2000.  
XX XX  
XX 24-NOV-1999; 99WO-US27863.  
XX PF  
XX 25-NOV-1998; 98US-0109938.  
XX PR  
XX (GEO ) GEN HOSPITAL CORP.  
XX PA  
XX Bringhurst FR, Takasu H, Gardella TJ, Potts JT;  
XX PI  
XX WPI; 2000-400076/34.  
XX DR  
XX Novel biologically active peptide comprising a parathyroid hormone  
XX peptide derivative, useful for treating osteoporosis -  
XX PT  
XX Disclosure; Page 69; 75pp; English.  
XX PS  
XX Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous  
CC cells, initiating signal transduction. It has been identified that the  
CC carboxyl terminal of PTH is important for PTH receptor binding, while the  
CC amino terminal is important for signal transduction. Various PTH peptides  
CC were produces with amino- and carboxy terminal modifications which had  
CC varying PTH receptor activation properties and therefore downstream  
CC signalling. Aberrant PTH activity has been implicated in a number of  
CC disorders: osteoporosis, osteopaenia, hypoparathyroidism and  
CC hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma  
CC and a variety of cancers: breast, lung and prostate carcinoma, multiple  
CC myeloma and epidermoid cancers of the head, neck and oesophagus. The  
CC present sequence is a PTH peptide, with a Gly residue at position 1 and  
CC a Glu residue at position 19. The Gly residue eliminates downstream  
CC signalling via phospholipase C (PLC) and the Glu residue reduces PLC  
CC signalling and ligand binding. PTH peptides with an Ala residue at  
CC position 1 and an Arg residue at position 19 have improved signalling  
CC properties and therefore may be suitable as PTH receptor agonists for the  
CC treatment of the above mentioned disorders and fracture repair.  
XX SQ Sequence 28 AA;

Query Match 97.8%; Score 134; DB 21; Length 28;  
Best Local Similarity 96.3%; Pred. No. 3.7e-13;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMXRVEWLKRL 28  
DB 2 vseiqmlhnlghklnsmervewlrkkl 28

RESULT 11  
AAY98052  
ID AAY98052 standard; peptide; 28 AA.  
XX AC  
XX AAY98052;  
XX DT  
XX 04-SEP-2000 (first entry)  
XX DE  
XX Human parathyroid hormone peptide # 12.  
XX KW  
XX Human; parathyroid hormone; signal transduction; osteoporosis;  
KW osteopaenia; hypoparathyroidism; fracture repair; hypercalcaemia;  
KW breast cancer; lung cancer; prostate cancer; multiple myeloma;  
KW hypernephroma; head and neck epidermoid cancer; oesophagus cancer;  
KW osteopathic; PTH.  
XX OS  
XX Homo sapiens.  
XX PN  
XX WO200031266-A1.  
XX XX  
XX 02-JUN-2000.  
XX PD

PF 24-NOV-1999; 99WO-US27863.  
XX PR  
XX 25-NOV-1998; 98US-0109938.  
XX XX  
XX (GEO ) GEN HOSPITAL CORP.  
XX PA  
XX Bringhurst FR, Takasu H, Gardella TJ, Potts JT;  
XX PI  
XX WPI; 2000-400076/34.  
XX DR  
XX Novel biologically active peptide comprising a parathyroid hormone  
XX peptide derivative, useful for treating osteoporosis -  
XX PT  
XX Disclosure; Page 69; 75pp; English.  
XX PS  
XX Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous  
CC cells, initiating signal transduction. It has been identified that the  
CC carboxyl terminal of PTH is important for PTH receptor binding, while the  
CC amino terminal is important for signal transduction. Various PTH peptides  
CC were produces with amino- and carboxy terminal modifications which had  
CC varying PTH receptor activation properties and therefore downstream  
CC signalling. Aberrant PTH activity has been implicated in a number of  
CC disorders: osteoporosis, osteopaenia, hypoparathyroidism and  
CC hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma  
CC and a variety of cancers: breast, lung and prostate carcinoma, multiple  
CC myeloma and epidermoid cancers of the head, neck and oesophagus. The  
CC present sequence is a PTH peptide, with a Gly residue at position 1 and  
CC a Glu residue at position 19. The Gly residue eliminates downstream  
CC signalling via phospholipase C (PLC) and the Glu residue reduces PLC  
CC signalling and ligand binding. PTH peptides with an Ala residue at  
CC position 1 and an Arg residue at position 19 have improved signalling  
CC properties and therefore may be suitable as PTH receptor agonists for the  
CC treatment of the above mentioned disorders and fracture repair.  
XX SQ Sequence 28 AA;

Query Match 97.8%; Score 134; DB 21; Length 28;  
Best Local Similarity 96.3%; Pred. No. 3.7e-13;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMXRVEWLKRL 28  
DB 2 vseiqmlhnlghklnsmervewlrkkl 28

RESULT 12  
AAR11731  
ID AAR11731 standard; Protein; 29 AA.  
XX AC  
XX AAR11731;  
XX DT  
XX 03-JUL-1991 (first entry)  
XX DE  
XX Adenine-rich PTH-(1-28) in pPTH-AA.  
XX KW  
XX Parathyroid hormone; calcium; osteoporosis; bone.  
XX OS  
XX Synthetic.  
XX PN  
XX WO9105050-A.  
XX PD  
XX 18-APR-1991.  
XX PF  
XX 01-OCT-1990; 90WO-C000335.  
XX XX  
XX 29-SEP-1989; 89CA-2615001.  
XX PR  
XX (CANA ) NAT RES COUNCIL CAN.  
XX PA  
XX Sung WL;  
XX PI  
XX WPI; 1991-132857/18.  
XX DR

DR N-PSDB; AAQ11617.  
 XX Mature human parathyroid synthesis - includes using eg E. coli  
 PT transformed by plasmid contg. synthetic nucleotide sequence contg.  
 PT adenine rich codons in N-terminal region.  
 XX  
 PS Disclosure; Fig 3; 62pp; English.  
 XX  
 CC The sequence is encoded by adenine rich codons. Codons 29-84  
 CC (see AAQ11618) are degenerate in the usage frequency favoured by  
 CC E.coli or yeast. A plasmid contg. the complete sequence expresses  
 CC PTH with an improved yield. PTH is a blood calcium regulator known  
 CC to increase bone mass.  
 XX  
 SQ Sequence 29 AA;  
 Query Match 97.8%; Score 134; DB 12; Length 29;  
 Best Local Similarity 96.3%; Pred. No. 3.8e-13;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 VSEIQLMHNLGKHLNSMXRVEWLRKKL 28  
 Db 3 vseiqimhnlghkhlmsmervewrkkl 29  
 RESULT 13  
 AAR88836  
 ID AAR88836 standard; peptide; 29 AA.  
 XX  
 AC AAR88836;  
 XX  
 DT 07-OCT-1996 (first entry)  
 XX  
 DE Human parathyroid hormone analogue, hPTH(1-29)-NH2.  
 XX  
 KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;  
 KW calcium regulation; reduced PKC activity; protein kinase C;  
 KW increased adenylyl cyclase activity; cAMPase; bone loss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 29 /note= "amidated"  
 FT  
 PN CA2126299-A.  
 XX  
 PD 21-DEC-1995.  
 XX  
 PF 20-JUN-1994; 94CA-2126299.  
 XX  
 PR 20-JUN-1994; 94CA-2126299.  
 XX  
 PA (WILL/) WILLICK G E.  
 XX  
 PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;  
 FT Willick GE;  
 FT  
 PN CA2126299-A.  
 XX  
 PD 21-DEC-1995.  
 XX  
 PF 20-JUN-1994; 94CA-2126299.  
 XX  
 PR 20-JUN-1994; 94CA-2126299.  
 XX  
 PA (WILL/) WILLICK G E.  
 XX  
 PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;  
 PI Willick GE;  
 XX  
 DR WPI; 1996-151754/16.  
 XX  
 PT New human parathyroid hormone analogues - which have increased  
 PT adenylyl cyclase activating activity, used for treating osteoporosis  
 XX  
 PS Claim 1; Fig 9; 21pp; English.  
 XX  
 CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The  
 CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)  
 CC activity and reduce protein kinase C (PKC) activity. The analogues  
 CC can reverse the loss of bone and increase bone mass and density  
 CC without undesirable effects. They are useful for the treatment of  
 CC osteoporosis and other bone related disorders and disorders  
 CC involving bone cell calcium regulation.

XX Sequence 29 AA;  
 SQ  
 Query Match 97.8%; Score 134; DB 17; Length 29;  
 Best Local Similarity 96.3%; Pred. No. 3.8e-13;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 VSEIQLMHNLGKHLNSMXRVEWLRKKL 28  
 Db 2 vseiqimhnlghkhlmsmervewrkkl 28  
 RESULT 14  
 AAR88832  
 ID AAR88832 standard; peptide; 30 AA.  
 XX  
 AC AAR88832;  
 XX  
 DT 07-OCT-1996 (first entry)  
 XX  
 DE Human parathyroid hormone analogue, hPTH(1-30)-NH2.  
 XX  
 KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;  
 KW calcium regulation; reduced PKC activity; protein kinase C;  
 KW increased adenylyl cyclase activity; cAMPase; bone loss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 30 /note= "amidated"  
 FT  
 PN CA2126299-A.  
 XX  
 PD 21-DEC-1995.  
 XX  
 PF 20-JUN-1994; 94CA-2126299.  
 XX  
 PR 20-JUN-1994; 94CA-2126299.  
 XX  
 PA (WILL/) WILLICK G E.  
 XX  
 PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;  
 PI Willick GE;  
 XX  
 DR WPI; 1996-151754/16.  
 XX  
 PT New human parathyroid hormone analogues - which have increased  
 PT adenylyl cyclase activating activity, used for treating osteoporosis  
 XX  
 PS Claim 1; Fig 5; 21pp; English.  
 XX  
 CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The  
 CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)  
 CC activity and reduce protein kinase C (PKC) activity. The analogues  
 CC can reverse the loss of bone and increase bone mass and density  
 CC without undesirable effects. They are useful for the treatment of  
 CC osteoporosis and other bone related disorders and disorders  
 CC involving bone cell calcium regulation.  
 XX  
 SQ Sequence 30 AA;  
 Query Match 97.8%; Score 134; DB 17; Length 30;  
 Best Local Similarity 96.3%; Pred. No. 4e-13;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 VSEIQLMHNLGKHLNSMXRVEWLRKKL 28  
 Db 2 vseiqimhnlghkhlmsmervewrkkl 28

Db 2 vseiqlmhnlghlnsmervewlrkkl 28

Search completed: August 31, 2001, 16:00:42  
Job time: 46 sec

RESULT 15  
AAW42059  
ID AAW42059 standard; peptide; 31 AA.  
XX  
AC AAW42059;  
XX  
DT 06-JUL-1998 (first entry)  
XX  
DE Human parathyroid hormone cyclic peptide analogue SEQ ID NO:14.  
XX  
KW Human; parathyroid hormone; hPTH; cyclic; osteoporosis; fracture;  
KW hypotensive action; bone.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 22 /note= "Glu is bound to Lys at position 26 to form  
FT a cyclic structure"  
FT Modified-site 26 /note= "Lys is bound to Glu at position 22 to form  
FT a cyclic structure"  
FT Modified-site 31 /note= "amidated"  
XX  
PN WO9805683-A1.  
XX  
PD 12-FEB-1998.  
XX  
PF 01-AUG-1997; 97WO-CA00547.  
XX  
PR 14-MAR-1997; 97US-0040560.  
PR 02-AUG-1996; 96US-0691647.  
XX  
PA (CANA ) NAT RES COUNCIL CANADA.  
XX  
PI Barbier J, Morley P, Neugebauer W, Ross V, Whitfield J;  
PI Willick GE;  
XX  
DR WPI; 1998-145550/13.  
XX  
PT Cyclic human parathyroid hormone peptide(s) with 27Lys substitution  
PT - for treating osteoporosis and fractures, also method for screening  
PT osteogenic peptide(s) based on their hypotensive action  
XX  
PS Claim 41; Fig 21; 77pp; English.  
XX  
CC The present sequence represents a human parathyroid hormone (hPTH)  
CC (1-31) peptide analogue. The present invention also describes a method  
CC for screening peptides for osteogenic activity by subcutaneous injection  
CC of a test compound and seeing if a small drop in arterial pressure  
CC occurs after a short time. The hPTH peptide analogue can be useful for  
CC stimulating bone growth, restoring bone and promoting bone healing,  
CC especially treatment of osteoporosis and normal fractures. The hPTH  
CC peptide analogue can be administered by injection or inhalation.  
CC rectally or orally, generally at at most 0.05 mg/kg/day. Substitution  
CC of Lys26 stabilises an alpha-helix in the receptor-binding region of  
CC the hormone and increases adenylyl cyclase (AC) activity, while  
CC cyclisation increases stability against proteases. The screening method,  
CC which can be performed in intact female animals, is a quick and simple  
CC way of identifying inactive compounds, avoiding the need for long-term,  
CC expensive tests on ovariectomised animals.  
XX  
SQ Sequence 31 AA;

Query Match 97.8%; Score 134; DB 19; Length 31;  
Best Local Similarity 96.3%; Pred. No. 4.1e-13;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 VSEIQLMHNIGKHLNSMVRVWLRKKL 28  
|||||





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 31, 2001, 15:59:56 ; Search time 21.89 Seconds  
(without alignments)  
169.234 Million cell updates/sec

Title: US-09-448-867-1  
Perfect score: 137  
Sequence: 1 XNSEIQLMNLGKHLNSMXRVEWLKKL 28

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL16:  
1: sp\_archaea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phase:  
10: sp\_plant:  
11: sp\_rodent:  
12: sp\_unclassified:  
13: sp\_vertebrate:  
14: sp\_virus:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	130	94.9	86	Q9NLV0	Q9nlv0 equus cabal
2	118	86.1	115	Q9GL67	Q9gl67 felis silve
3	117	85.4	115	Q9ZOL6	Q9z016 mus musculu
4	60	43.8	163	Q918E9	Q9i8e9 fugu rubrip
5	56	40.9	162	Q918U2	Q9i8u2 sparus aura
6	50.5	36.9	303	Q9VIA4	Q9via4 drosophila
7	50.5	36.9	711	Q24164	Q24164 drosophila
8	50.5	36.9	785	Q9NBK6	Q9nbk6 drosophila
9	50	36.5	336	Q9K7V5	Q9k7v5 bacillus ha
10	50	36.5	1500	Q9VLQ8	Q9vlq8 drosophila
11	49	35.8	63	Q9LH68	Q9lh68 arabidopsis
12	49	35.8	115	Q9YD49	Q9yd49 aeropyrum p
13	49	35.8	244	Q9N4T2	Q9n4t2 caenorhabdi
14	49	35.8	977	Q9U0H9	Q9u0h9 plasmodium
15	47	34.3	207	Q25713	Q25713 helicobacte
16	47	34.3	256	P91490	P91490 caenorhabdi
17	47	34.3	326	Q9U8W5	Q9u8w5 eptatretus
18	47	34.3	339	Q17633	Q17633 caenorhabdi
19	47	34.3	345	Q9PVU7	Q9pvu7 lampetra re

20	47	34.3	386	3	P79004	P79004 saccharomyc
21	47	34.3	758	5	Q9W0E8	Q9w0e8 drosophila
22	47	34.3	1048	13	P79749	P79749 fugu rubrip
23	46.5	33.9	544	2	Q9X3R2	Q9x3r2 pseudomonas
24	46.5	33.9	790	5	Q9VIK6	Q9vik6 drosophila
25	46	33.6	111	10	Q42354	Q42354 arabidopsis
26	46	33.6	121	6	Q9GK30	Q9gk30 oviz aries
27	46	33.6	124	7	Q31524	Q31524 poecilia re
28	46	33.6	177	6	Q9GLC7	Q9glc7 oryctolagus
29	46	33.6	285	7	Q31521	Q31521 poecilia re
30	46	33.6	297	2	Q9KNJ6	Q9knj6 vibrio chol
31	46	33.6	313	7	Q31523	Q31523 poecilia re
32	46	33.6	323	10	Q9ZU32	Q9zu32 arabidopsis
33	46	33.6	353	2	P97053	P97053 pseudomonas
34	46	33.6	401	13	Q9U8U9	Q9u8u9 eptatretus
35	46	33.6	457	13	Q90269	Q90269 brachydanio
36	46	33.6	490	10	Q24430	Q24430 glycine max
37	46	33.6	495	10	Q39016	Q39016 arabidopsis
38	46	33.6	501	10	Q38869	Q38869 arabidopsis
39	46	33.6	557	10	Q9LQH7	Q9lqh7 arabidopsis
40	46	33.6	733	11	Q9QZM7	Q9qzm7 mus musculu
41	46	33.6	1059	13	Q9DE49	Q9de49 brachydanio
42	46	33.6	1087	13	Q9PUF6	Q9puf6 gallus gall
43	45	32.8	96	14	Q89625	Q89625 human immun
44	45	32.8	172	13	Q91177	Q91177 oryzias lat
45	45	32.8	172	13	Q02528	Q02528 oryzias lat

## ALIGNMENTS

RESULT 1

Q9NLV0 PRELIMINARY; PRT; 86 AA.  
AC Q9NLV0:  
DT 01-OCT-2000 (TRENBLrel. 15, Created)  
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)  
DE PARATHYROID HORMONE (FRAGMENT).  
GN PTH.  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20082971; PubMed=10613847;  
RA Caetano A.R., Shue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,  
Bowling A.T., Murray J.D.;  
RT "A comparative gene map of the horse (Equus caballus).";  
RL Genome Res. 9:1239-1249(1999).  
DR EMBL: AF134233; AAF62347.1; -;  
DR InterPro: IPR001415; -;  
DR Pfam: PF01279; Parathyroid; 1.  
DR PROSITE: PS00335; PARATHYROID; 1.  
FT NON\_TER 1  
SQ SEQUENCE 86 AA; 9805 MW; 253184EA681A2022 CRC64;

Query Match 94.9%; Score 130; DB 6; Length 86;  
Best Local Similarity 92.6%; Pred. No. 2.5e-12;  
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQLMNLGKHLNSMXRVEWLKKL 28 ✓

DB 4 VSEIQLMNLGKHLNSMXRVEWLKKL 30

RESULT 2 OK

Q9GL67 PRELIMINARY; PRT; 115 AA.

ID Q9GL67

AC Q9GL67;  
DT 01-MAR-2001 (TRENBLrel. 16, Created)

Query Match	40.9%;	Score 56;	DB 13;	Length 162;
Best Local Similarity	44.4%;	Pred. No. 0.67;		

Matches 12; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 2 VSEIQLMHNIGKHLNSKXRVWLRKLL 28  
 || ||||: | | | | | ||: |  
 Db 39 VSHAQLMHDKGRSLQEFKRRMRLHELL 65

RESULT 6  
 Q9VIA4 PRELIMINARY; PRT; 303 AA.  
 AC Q9VIA4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE MSTPROX PROTEIN.  
 GN MSTPROX OR CG1149.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY.  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,  
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadien E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA De Paulos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleab J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AE003672; AAF54021.1; -;  
 DR FlyBase; FBgn0015770; MstProx.  
 DR InterPro; IPR000372; -;  
 DR Pfam; PF01462; LRRNT; 1.  
 DR SMART; SM00013; LRRNT; 1.  
 SQ SEQUENCE 303 AA; 35689 MW; 57BA402F6AF764D5 CRC64;

Query Match 36.9%; Score 50.5; DB 5; Length 303;  
 Best Local Similarity 29.4%; Pred. No. 8.8;

Matches 10; Conservative 10; Mismatches 7; Indels 7; Gaps 1;

QY 2 VSEIQLMHNIGKHLNSKXRV-----EWLRKLL 28  
 || ||||: | | | | | ||: |  
 Db 213 INEQLLQSMHRKLNLTMSIYKMEWLHRKL 246

RESULT 7  
 Q24164 PRELIMINARY; PRT; 711 AA.  
 AC Q24164;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE DMSTPROX.  
 GN MSTPROX OR CG1149.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96215042; PubMed=8621445;  
 RA Mitcham J.L., Parnet P., Bonnett T.P., Garka K.E., Gerhart M.J.,  
 RA Slack J.L., Gayle M.A., Dower S.K., Sims J.E.;  
 RT "J1/Sr2 signaling establishes it as a member of an expanding  
 RT interleukin-1 receptor family.";  
 RL J. Biol. Chem. 271:5777-5783(1996).  
 DR EMBL; U42425; AAC46999.1; -;  
 DR FlyBase; FBgn0015770; MstProx.  
 DR InterPro; IPR000157; -;  
 DR InterPro; IPR000372; -;  
 DR InterPro; IPR001611; -;  
 DR Pfam; PF00560; LRR; 2.  
 DR Pfam; PF01462; LRRNT; 1.  
 DR Pfam; PF01582; TIR; 1.  
 DR SMART; SM00255; TIR; 1.  
 SQ SEQUENCE 711 AA; 83175 MW; 007CD7AEF67BC1B0 CRC64;

Query Match 36.9%; Score 50.5; DB 5; Length 711;  
 Best Local Similarity 29.4%; Pred. No. 22;  
 Matches 10; Conservative 10; Mismatches 7; Indels 7; Gaps 1;

QY 2 VSEIQLMHNIGKHLNSKXRV-----EWLRKLL 28  
 || ||||: | | | | | ||: |  
 Db 213 INEQLLQSMHRKLNLTMSIYKMEWLHRKL 246

RESULT 8  
 Q9NBK6 PRELIMINARY; PRT; 785 AA.  
 AC Q9NBK6;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE TOLL-3 (FRAGMENT).  
 GN MSTPROX OR CG1149.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tauszig S., Jouanguy E., Hoffmann J., Imber J.L.;  
 RT "Toll-related receptors and the control of antimicrobial peptide  
 RT expression in Drosophila.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2000).  
 DR EMBL; AF247769; AAF86229.1; -;  
 DR FlyBase; FBgn0015770; MstProx.  
 DR InterPro; IPR000157; -;

RESULT	ID	PRELIMINARY	PRT	63 AA.
11	Q9LH68			
	AC	Q9LH68		
	DT	01-OCT-2000 (TREMBLrel. 15, Created)		
	DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
	DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)		
	DE	GB AD27902.1.		
	OS	Arabisopsis thaliana (Mouse-ear cress).		
	OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
	OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;		
	OC	Brassicales; Brassicaceae; Arabidopsis.		

```

OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
  investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
SQ SEQUENCE 63 AA; 7025 MW; 2C8966DDEB4673DD CRC64;

Query Match 35.8%; Score 49; DB 10; Length 63;
Best Local Similarity 47.1%; Pred. No. 2.8; Mismatches 5; Indels 0; Gaps 0;
Matches 8; Conservative 4;

QY 7 LMHNLGKHLNSMXRVEV 23
Db 38 LLNLGKHPNKVIQTVW 54
I:|||||I:|

RESULT 12
Q9YD49 PRELIMINARY; PRT; 115 AA.
ID Q9YD49;
AC Q9YD49;
DF 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE HYPOTHETICAL 12.6 KDA PROTEIN APE1063.
GN APE1063.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
OC Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
  Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankaï A., Kosugi H.,
  Hosoyama A., Fukui Y., Nagai Y., Nishijima K., Nakazawa H.,
  Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
  Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
  Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
  crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
DR EMBL; AP000060; BAA80048.1;
KW Hypothetical protein.
SQ SEQUENCE 115 AA; 12603 MW; D9A02D3E1D5CC232 CRC64;

Query Match 35.8%; Score 49; DB 1; Length 115;
Best Local Similarity 40.7%; Pred. No. 5.3; Mismatches 10; Indels 0; Gaps 0;
Matches 11; Conservative 6;

QY 2 VSEIQLMHNGLGKHLNSMXRVEVLRKKL 28
Db 18 VAALYLHLRLGPTLYNGEAVILRL 44
I:|||||I:|||||I:|

RESULT 13
Q9N4T2 PRELIMINARY; PRT; 244 AA.
ID Q9N4T2;
AC Q9N4T2;
DF 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Y50D4B.B PROTEIN.
GN Y50D4B.B.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
  investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
SQ SEQUENCE FROM N.A.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX Lamar B., Le T.;
RT "The sequence of C. elegans cosmid Y50D4B.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX Waterston R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006795; AAF59493.1;
DR InterPro; IPR001245;
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
DR SMART; SM00219; Tykrc; 1.
KW ATP-binding; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 244 AA; 28568 MW; C389C56F7E31524A CRC64;

Query Match 35.8%; Score 49; DB 5; Length 244;
Best Local Similarity 36.4%; Pred. No. 12; Mismatches 8; Indels 0; Gaps 0;
Matches 8; Conservative 6;

QY 4 EIQLMHNGLGKHLNSMXRVEVLR 25
Db 37 ELNVNCVVGKHPNLIILIRWIR 58
I:|:|:|I:|:|:|I:|

RESULT 14
Q9U0H9 PRELIMINARY; PRT; 977 AA.
ID Q9U0H9;
AC Q9U0H9;
DF 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE HYPOTHETICAL 117.5 KDA PROTEIN.
GN MAL4P2.43.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX Devlin K., Bowman S., Churcher C., Harris B., Lawson D.,
  Quail M., Barrell B.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035475; CAB62884.1;
KW Hypothetical protein.
SQ SEQUENCE 977 AA; 117527 MW; 3FBE5600D7A0F61D CRC64;

Query Match 35.8%; Score 49; DB 5; Length 977;
Best Local Similarity 33.3%; Pred. No. 51; Mismatches 9; Indels 2; Gaps 1;
Matches 8; Conservative 9;

QY 2 VSEIQLMHNGLGKHLNSMXRVEVLR 25
Db 365 ILEKIMHNRNKHLEK--KIEFIK 386
I:|:|:|I:|I:|:|:|

RESULT 15

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025713
ID O25713 PRELIMINARY; PRT; 207 AA.
AC O25713;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE HYPOTHETICAL 23.7 KDA PROTEIN.
GN HP1081.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RA MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
pylori."
RL Nature 388:539-547(1997).
DR EMBL; AE000615; AAD08133.1; -.
DR TIGR; HP1081; -.
KW Hypothetical protein.
SQ SEQUENCE 207 AA; 23737 MW; 9BF3A0E76590AB37 CRC64;

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Query Match 34.3%; Score 47; DB 2; Length 207;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

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QY 7 LMHNLGKHLNSMXRVEWL 24
   ||| |||
Db 190 LMEGLEKRLNAIKNAEWL 207

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Search completed: August 31, 2001, 16:01:30  
Job time: 94 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 31, 2001, 15:59:56 ; Search time 10.02 Seconds  
(without alignments)  
95,724 Million cell updates/sec

Title: US-09-448-867-1  
Perfect score: 137  
Sequence: 1 XVSEIQLMHNGLKHLNSMXRVEWLKRL 28

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	134	97.8	115	1 PTHY_HUMAN	P01270 homo sapien
2	134	97.8	115	1 PTH_MACEA	Q9xt35 macaca fasc
3	126	92.0	115	1 PTHY_PIG	P01269 sus scrofa
4	125	91.2	115	1 PTHY_BOVIN	P01268 bos taurus
5	125	91.2	115	1 PTHY_CANFA	P52212 canis fami
6	116	84.7	115	1 PTHY_RAT	P04089 rattus norv
7	90	65.7	119	1 PTHY_CHICK	P15743 gallus gall
8	54	39.4	824	1 STL_THEMA	Q9wy15 thermotoga
9	52	38.0	363	1 MORG_BORBU	O51708 borrelia bu
10	51	37.2	564	1 GAF2_SCHPO	Q10134 schizosacch
11	50.5	36.9	508	1 GDFK_SOYBN	P28583 glycine max
12	50	36.5	848	1 TORA_ECOLI	P33225 escherichia
13	47	34.3	1098	1 PGDR_MOUSE	P05622 mus musculu
14	47	34.3	1106	1 PGDR_HUMAN	P09619 homo sapien
15	46	33.6	175	1 PTHR_MOUSE	P22858 mus musculu
16	46	33.6	176	1 PTHR_CHICK	P17251 gallus gall
17	46	33.6	177	1 PTHR_CANFA	P52211 canis fami
18	46	33.6	177	1 PTHR_HUMAN	P12272 homo sapien
19	46	33.6	177	1 PTHR_RAT	P13085 rattus norv
20	46	33.6	182	1 FRIL_RAT	P02793 rattus norv
21	46	33.6	211	1 LOLA_COXBU	P39917 coxiella bu
22	46	33.6	224	1 AZRL_SCHPO	Q09189 schizosacch
23	46	33.6	538	1 PYRG_HELPJ	Q9zm99 helicobacte
24	46	33.6	538	1 PYRG_HELPY	O25116 helicobacte
25	46	33.6	1087	1 PGDS_MOUSE	P28619 xenopus lae
26	46	33.6	1088	1 PGDS_RAT	P20786 rattus norv
27	46	33.6	1089	1 PGDS_HUMAN	P16234 homo sapien
28	46	33.6	1089	1 PGDS_MOUSE	P26618 mus musculu
29	45.5	33.2	528	1 YJCC_ECOLI	P32701 escherichia
30	45	32.8	631	1 MERA_BACSR	P16171 bacillus sp
31	45	32.8	654	1 BFR2_HUMAN	Q01742 homo sapien
32	45	32.8	801	1 FGR3_MOUSE	Q61851 mus musculu
33	45	32.8	806	1 CEK2_CHICK	P18460 gallus gall

34 45 32.8 806 1 FGR3\_HUMAN P22607 homo sapien  
35 45 32.8 813 1 FGR2\_XENLA Q03364 xenopus lae  
36 45 32.8 821 1 FGR2\_HUMAN P21802 homo sapien  
37 45 32.8 821 1 FGR2\_MOUSE P21803 mus musculu  
38 45 32.8 823 1 CEK3\_CHICK P18461 gallus gall  
39 44.5 32.5 556 1 KNLC\_RAT P37285 rattus norv  
40 44.5 32.5 569 1 KNLC\_HUMAN Q07866 homo sapien  
41 44 32.1 182 1 FRIL\_MOUSE P29391 mus musculu  
42 44 32.1 182 1 FRIL\_MOUSE P49945 mus musculu  
43 44 32.1 199 1 SODF\_RHIME Q9xd74 rhizobium m  
44 44 32.1 246 1 SRIA\_PHYPO P09350 physarum po  
45 44 32.1 300 1 ALF1\_SYNY3 P74309 synechocyst

#### ALIGNMENTS

RESULT 1  
PTHY\_HUMAN  
ID PTHY\_HUMAN STANDARD; PRT; 115 AA.  
AC P01270;  
DC 21-JUL-1986 (Rel. 01, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH) (PARATHORMONE).  
GN PTH.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82150870; PubMed=6950381;  
RA Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;  
RT "Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.";  
RL Proc. Natl. Acad. Sci. U.S.A. 78:7365-7369(1981).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83169834; PubMed=6220408;  
RA Vasicek T.J., McDevitt B.E., Freeman M.W., Fennick B.J.,  
RA Hendy G.N., Potts J.T. Jr., Rich A., Kronenberg H.M.;  
RT "Nucleotide sequence of the human parathyroid hormone gene.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).  
RN [3]  
RP SEQUENCE OF 26-37.  
RX MEDLINE=74174967; PubMed=4833516;  
RA Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;  
RT "Structural analysis of human parathyroid hormone by a new microsequencing approach.";  
RL Nature 249:155-157(1974).  
RN [4]  
RP SEQUENCE OF 32-68.  
RX MEDLINE=7411056; PubMed=4521809;  
RA Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,  
RA O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;  
RT "The amino-acid sequence of the amino-terminal 37 residues of human parathyroid hormone.";  
RL Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974).  
RN [5]  
RP SEQUENCE OF 61-83 AND 84-115.  
RX MEDLINE=79082855; PubMed=728431;  
RA Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,  
RA Potts J.T. Jr.;  
RT "Complete amino acid sequence of human parathyroid hormone.";  
RL Biochemistry 17:5723-5729(1978).  
RN [6]  
RP SEQUENCE OF 75-100.  
RA Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N.,  
RA O'Riordan J.L.H., Potts J.T. Jr.;  
RL (in) Talmadge R.V., Owen M., Parsons J.A. (eds.);  
RL Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation, Amsterdam (1975).



[7]  
RN REVISIONS.  
RX MEDLINE=75146516; PubMed=1125201;  
RA Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;  
RT "A reinvestigation of the amino-terminal sequence of human  
RL parathyroid hormone."  
RN Biochemistry 14:1842-1847(1975).  
[8]  
RN SYNTHESIS OF 32-65.  
RX MEDLINE=75059220; PubMed=4474131;  
RA Tregear G.W., van Rietschoten J., Green E., Niall H.D.,  
RX Keutmann H.T., Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;  
RT "Solid-phase synthesis of the biologically active N-terminal 1-34  
RL peptide of human parathyroid hormone."  
RN Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).  
[9]  
RN SYNTHESIS OF 32-65.  
RX MEDLINE=73227467; PubMed=4721748;  
RA Andreatta R.H., Hartmann A., Joehl A., Kamber B., Maier R.,  
RA Riniker B., Rittel W., Sieber P.;  
RT "Synthesis of sequence 1-34 of human parathyroid hormone."  
RN Helv. Chim. Acta 56:470-473(1973).  
[10]  
RN STRUCTURE BY NMR OF 32-65.  
RX MEDLINE=91299748; PubMed=2069952;  
RA Klaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer H.;  
RT "Investigation of the solution structure of the human parathyroid  
RL hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry,  
RN and molecular dynamics calculations."  
RX Biochemistry 30:6936-6942(1991).  
[11]  
RN STRUCTURE BY NMR OF 32-65.  
RX MEDLINE=93345518; PubMed=8344299;  
RA Barden J.A., Cuthbertson R.M.;  
RT "Stabilized NMR structure of human parathyroid hormone(1-34).";  
RN Eur. J. Biochem. 215:315-321(1993).  
[12]  
RN STRUCTURE BY NMR OF 32-68.  
RX MEDLINE=95318084; PubMed=7797503;  
RA Marx U.C., Austermann S., Bayer P., Adermann K., Echart A.,  
RA Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,  
RA Roesch P.;  
RT "Structure of human parathyroid hormone 1-37 in solution."  
RN J. Biol. Chem. 270:15194-15202(1995).  
[13]  
RN STRUCTURE BY NMR OF 32-70.  
RX MEDLINE=20090619; PubMed=10623601;  
RA Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;  
RT "Solution structures of human parathyroid hormone fragments  
RL hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment  
RN bPTH(1-37)."  
RX Biochem. Biophys. Res. Commun. 267:213-220(2000).  
[14]  
RN VARIANT ARG-18.  
RX MEDLINE=91009811; PubMed=2212001;  
RA Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,  
RA Kronenberg H.M.;  
RT "Mutation of the signal peptide-encoding region of the  
RL preproparathyroid hormone gene in familial isolated  
RN hypoparathyroidism."  
RX J. Clin. Invest. 86:1084-1087(1990).  
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
CC BONE AND PREVENTING THEIR RENAL EXCRETION.  
CC -1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED  
CC HYPOPARATHYROIDISM (FIH).  
CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.  
CC  
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CC  
CC EMBL; J00301; AAA60215.1; -;  
DR EMBL; V00597; CAA23843.1; -;  
DR EMBL; A29146; CAA01956.1; -;  
DR PIR; A01536; PTHU.  
DR PIR; A19339; A19339.  
DR PDB; 1HPH; 10-JUL-95.  
DR PDB; 1HTH; 15-OCT-97.  
DR PDB; 1ZWA; 12-MAR-97.  
DR PDB; 1ZWB; 12-MAR-97.  
DR PDB; 1ZWD; 12-MAR-97.  
DR PDB; 1ZWE; 12-MAR-97.  
DR PDB; 1ZWF; 16-JUN-97.  
DR PDB; 1ZWG; 16-JUN-97.  
DR PDB; 1BWV; 14-JAN-00.  
DR PDB; 1HPY; 14-JAN-00.  
DR MIM; 146200; -;  
DR MIM; 168450; -;  
DR InterPro; IPR001415; -;  
DR Pfam; PF01279; Parathyroid; 1.  
DR PROSITE; PS00335; PARATHYROID; 1.  
KW Hormone; Signal; Disease mutation; 3D-structure.  
FT SIGNAL 1 25  
FT PROPEP 26 31  
FT CHAIN 32 115  
FT VARIANT 18 18  
FT C -> R (IN FIH; LEADS TO INEFFICIENT  
FT PROCESSING OF THE PRECURSOR).  
FT /FTid=VAR\_006047.  
FT CONFLICT 107 107 N -> D (IN REF. 5).  
FT SEQUENCE 115 AA; 12861 MW; 849015736AE5597 CRC64;  
Query Match 97.8%; Score 134; DB 1; Length 115;  
Best Local Similarity 96.3%; Pred. No. 2.3e-13;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 VSEIQLMHNKGLNSMXRVLEWLRKLL 28  
DB 33 VSEIQLMHNKGLNSMERVLEWLRKLL 59  
RESULT 2  
PTH\_MACFA  
ID PTH\_MACFA STANDARD; PRT; 115 AA.  
AC Q9XT35;  
DT 01-OCT-2000 (Rel. 40, Created)  
DT 01-OCT-2000 (Rel. 40, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).  
GN PTH.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Malaivijitnond S.; Takenaka O.;  
RT "Nucleotide sequences of parathyroid gene in five species of macaque  
RL of Thailand."  
RL J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).  
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN  
CC BONE AND PREVENTING THEIR RENAL EXCRETION.  
CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.  
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CC -----
DR EMBL; AF130257; AAD42777.1; -.
DR HSSP; P01270; IHPY.
DR InterPro; IPR001415; -.
DR Pfam; PF01279; Parathyroid; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal.
FT SIGNAL 1 25 BY SIMILARITY.
FT PROPEP 26 31 BY SIMILARITY.
FT CHAIN 32 115 PARATHYROID HORMONE.
SQ SEQUENCE 115 AA; 12890 MW; 8C2500EF24BE5597 CRC64;

Query Match 97.8%; Score 134; DB 1; Length 115;
Best Local Similarity 96.3%; Pred. No. 2.3e-13;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQLMNLGKHLNSMXRVLELRKKL 28
DB 33 VSEIQLMNLGKHLNSMXRVLELRKKL 59

RESULT 3
PTHY_PIG
ID PTHY_PIG STANDARD; PRT; 115 AA.
AC P01269;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87316938; PubMed=3628009;
RA Schmelzer H.-J., Gross G., Wildera G., Mayer H.;
RT "Nucleotide sequence of a full-length cDNA clone encoding
preproparathyroid hormone from pig and rat.";
RL Nucleic Acids Res. 15:6740-6740(1987).
RN [2]
RP SEQUENCE OF 26-115.
RX MEDLINE=76018954; PubMed=1164500;
RA Chu L.L.H., Huang W.-Y., Littlelike E.T., Hamilton J.W., Cohn D.V.;
RT "Porcine parathyroid hormone. Identification, biosynthesis, and
partial amino acid sequence.";
RL Biochemistry 14:3631-3635(1975).
RN [3]
RP SEQUENCE OF 32-115.
RX MEDLINE=74253317; PubMed=4840833;
RA Sauer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,
RA Potts J.T. Jr.;
RT "The amino acid sequence of porcine parathyroid hormone.";
RL Biochemistry 13:1994-1999(1974).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X05722; CAA29193.1; -.
DR PIR; A01535; PTPG.
DR PIR; B26806; B26806.
DR HSSP; P01270; IHPH.
DR InterPro; IPR001415; -.

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DR Pfam; PF01279; Parathyroid; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
SQ SEQUENCE 115 AA; 12852 MW; 9F8BBCDE614BAC16 CRC64;

Query Match 92.0%; Score 126; DB 1; Length 115;
Best Local Similarity 88.9%; Pred. No. 3.7e-12;
Matches 24; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQLMNLGKHLNSMXRVLELRKKL 28
DB 33 VSEIQLMNLGKHLNSMXRVLELRKKL 59

RESULT 4
PTHY_BOVIN
ID PTHY_BOVIN STANDARD; PRT; 115 AA.
AC P01268;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80056617; PubMed=388425;
RA Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,
RA Potts J.T. Jr., Rich A.;
RT "Cloning and nucleotide sequence of DNA coding for bovine
preproparathyroid hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=82037785; PubMed=6170060;
RA Weaver C.A., Gordon D.F., Kemper B.;
RT "Introduction by molecular cloning of artifactual inverted sequences
at the 5' terminus of the sense strand of bovine parathyroid hormone
cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=83105964; PubMed=6185374;
RA Weaver C.A., Gordon D.F., Kemper B.;
RT "Nucleotide sequence of bovine parathyroid hormone messenger RNA.";
RL Mol. Cell. Endocrinol. 28:411-424(1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=84262483; PubMed=6086460;
RA Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
RT "Isolation and complete nucleotide sequence of the gene for bovine
parathyroid hormone.";
RL Gene 28:319-329(1984).
RN [5]
RP SEQUENCE OF 26-115.
RX MEDLINE=74142666; PubMed=4522780;
RA Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,
RA Cohn D.V.;
RT "The N-terminal amino-acid sequence of bovine parathyroid
hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).
RN [6]
RP SEQUENCE OF 32-115.
RX MEDLINE=71076162; PubMed=5531031;
RA Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,

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RA Aurbach G.D., Potts J.T. Jr.;
RT "The amino acid sequence of bovine parathyroid hormone I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).
RN [7]
RP SEQUENCE OF 32-115.
RX MEDLINE=71063634; PubMed=5275384;
RA Brewer H.B. Jr., Ronan R.;
RT "Bovine parathyroid hormone: amino acid sequence.";
RN Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).
RX [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE=71091598; PubMed=4322265;
RA Potts J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,
RA Deftos L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;
RT "Synthesis of a biologically active N-terminal tetraacetate peptide
of parathyroid hormone.";
RN Proc. Natl. Acad. Sci. U.S.A. 68:63-67(1971).
RX [9]
RP STRUCTURE BY NMR OF 32-68.
RX MEDLINE=20090619; PubMed=10623601;
RA Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
RT "Solution structures of human parathyroid hormone fragments
bPTH(1-34) and bPTH(1-39) and bovine parathyroid hormone fragment
bPTH(1-37).";
RN Biochem. Biophys. Res. Commun. 267:213-220(2000).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC -----
DR EMBL; Y00106; CAA23439.1; -
DR EMBL; J00024; AAA30747.1; -
DR EMBL; K01938; AAA30749.1; -
DR EMBL; M25082; AAA30748.1; -
DR PIR; A01534; PTBO.
DR PIR; A24949; A24949.
DR PDB; 1ZWC; 12-MAR-97.
DR InterPro; IPR001415; -
DR Pfam; PF01279; Parathyroid; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal; 3D-structure.
FT SIGNAL 1 25
FT PROPEP 26 31 PARATHYROID HORMONE.
FT CHAIN 32 115
FT CONFLICT 106 106 V -> G (IN REF. 4).
SQ SEQUENCE 115 AA; 12980 MW; 2ED246B348880710 CRC64;

Query Match 91.2%; Score 125; DB 1; Length 115;
Best Local Similarity 88.9%; Pred. No. 5.2e-12;
Matches 24; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMXRVEWLKKL 28
DB 33 VSEIQFMHNLGKHLSSMERVEWLKKL 59

RESULT 5
PTHY_CANFA
ID PTHY_CANFA STANDARD; PRT; 115 AA.
AC P52212;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.

Query Match 91.2%; Score 125; DB 1; Length 115;
Best Local Similarity 88.9%; Pred. No. 5.2e-12;
Matches 24; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMXRVEWLKKL 28
DB 33 VSEIQFMHNLGKHLSSMERVEWLKKL 59

RESULT 6
PTHY_RAT
ID PTHY_RAT STANDARD; PRT; 115 AA.
AC P04089; Q63473;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84135846; PubMed=6321505;
RA Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;
RT "Gene encoding parathyroid hormone. Nucleotide sequence of the rat
gene and deduced amino acid sequence of rat preproparathyroid
hormone.";
RN J. Biol. Chem. 259:3320-3329(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87316938; PubMed=3628009;
RA Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT "Nucleotide sequence of a full-length cDNA clone encoding
preproparathyroid hormone from pig and rat.";

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OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Parathyroid;
RX MEDLINE=95369696; PubMed=7642102;
RA Rosol T.J., Steinmeyer C.L., McCauley L.K., Groene A.,
RA Dewille J.W., Capen C.C.;
RT "Sequences of the cDNAs encoding canine parathyroid hormone-related
protein and parathyroid hormone.";
RL Gene 160:241-243(1995).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC -----
DR EMBL; U15662; AAA82584.1; -
DR HSP; P01270; 1ZWC.
DR InterPro; IPR001415; -
DR Pfam; PF01279; Parathyroid; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal.
FT SIGNAL 1 25 BY SIMILARITY.
FT PROPEP 26 31 BY SIMILARITY.
FT CHAIN 32 115 PARATHYROID HORMONE.
SQ SEQUENCE 115 AA; 12957 MW; FC38F77F1C8CF56 CRC64;

Query Match 91.2%; Score 125; DB 1; Length 115;
Best Local Similarity 88.9%; Pred. No. 5.2e-12;
Matches 24; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMXRVEWLKKL 28
DB 33 VSEIQFMHNLGKHLSSMERVEWLKKL 59

RESULT 6
PTHY_RAT
ID PTHY_RAT STANDARD; PRT; 115 AA.
AC P04089; Q63473;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84135846; PubMed=6321505;
RA Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;
RT "Gene encoding parathyroid hormone. Nucleotide sequence of the rat
gene and deduced amino acid sequence of rat preproparathyroid
hormone.";
RN J. Biol. Chem. 259:3320-3329(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87316938; PubMed=3628009;
RA Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT "Nucleotide sequence of a full-length cDNA clone encoding
preproparathyroid hormone from pig and rat.";

```



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genome sequence of Thermotoga maritima.";
RT
Nature 399:323-329(1999).
RL
-!- CATALYTIC ACTIVITY: ATP + L-LEUCINE + TRNA(LEU) = AMP +
CC
PYROPHOSPHATE + L-LEUCYL-TRNA(LEU).
CC
-!- SUBCELLULAR LOCATION: CYTOSOLASMIC.
CC
-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC
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EMBL; AE001702; AAD35261.1; -.
DR
TIGR; TM0168; -.
DR
InterPro; IPR002300; -.
DR
InterPro; IPR002302; -.
DR
Pfam; PF00133; trna-synt_1; 1.
DR
PRINTS; P000985; TRNAsYNTHLEU.
DR
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT
SITE 41 51
FT
"HIGH" REGION.
FT
SITE 580 584
FT
"RMSKS" REGION.
FT
BINDING 583 583
FT
ATP (BY SIMILARITY).
SQ
SEQUENCE 824 AA; 95624 MW; 7C80252A76A844EC CRC64;

```

```
Query Match      39.4%; Score 54; DB 1; Length 824;
Best Local Similarity 41.7%; Pred. No. 1.7;
Matches 10; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
```

RESULT	9
MURG_BORBU	
ID	MURG_BORBU STANDARD; PRT; 363 AA.
AC	O51708;
DT	30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DE	UDP-N-ACETYLGLUCOSAMINE--N-ACETYLMURAMYL-(PENTAPEPTIDE)
DE	PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGALACTOSAMINE TRANSFERASE
DE	(EC 2.4.1.-) (UNDECAPRENYL-PP-MURNAC-PENTAPEPTIDE-UDPGLCNAC GLCNAC
DE	TRANSFERASE)
GN	MURG OR BBO767.
OS	Borrelia burgdorferi ( Lyme disease spirochete).
OS	Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX	NCBI_TaxID=139;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-ATCC 35210 / B31;
RX	MEDLINE=98065543; PubMed=9403685;
RA	Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA	Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA	Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA	Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA	van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA	Utterback T., Watney L., McDonald L., Artlich P., Bowman C.,
RA	Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA	Smith H.O., Venter J.C.;
RT	"Genomic sequence of a Lyme disease spirochaete, Borrelia
RL	burgdorferi.";
RL	Nature 390:580-586(1997).
-!	-!- FUNCTION: CELL WALL FORMATION. CATALYZES THE TRANSFER OF A GLCNAC
CC	SUBUNIT ON UNDECAPRENYL-PYROPHOSPHORYL-MURNAC-PENTAPEPTIDE (LIPID
CC	INTERMEDIATE I) TO FORM UNDECAPRENYL-PYROPHOSPHORYL-MURNAC-
CC	(PENTAPEPTIDE)GLCNAC (LIPID INTERMEDIATE II) (BY SIMILARITY).
CC	-!- PATHWAY: LAST STEP OF PEPTIDOGLYCAN BIOSYNTHESIS.

```
CC CC -!- SUBCELLULAR LOCATION: MEMBRANE ASSOCIATED (BY SIMILARITY).  
CC CC -!- SIMILARITY: BELONGS TO THE MURG FAMILY.  
-----  
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CC or send an email to license@isb-sib.ch).  
-----  
DR EMBL; AE001176; AAC67113.1; -.  
DR TIGR; BB9767; .  
KW Transferase; Glycosyltransferase; Cell division; Cell wall;  
KW Membrane; Peptidoglycan synthesis.  
SQ SEQUENCE 363 AA; 41118 MW; 1BAFA347384DB235 CRC64;  
  
Query Match          38.0%; Score 52; DB 1; Length 363;  
Best Local Similarity 36.0%; Pred. No. 1.5;  
Matches    9; Conservative   7; Mismatches     9; Indels      0; Gaps      0;  
  
QY              3 SEQLMHLNGLKSLNSXMRVLELRKK 27.  
                  ::::|:::::  
Db             217 AEIYFIHQSKNLNDISEKNYLRRQ 241  
                  ::::|:::::  
  
RESULT 10  
GAF2_SCHPO  
ID  GAF2_SCHPO STANDARD; PRT; 564 AA.  
AC Q10134;  
DT 01-FEB-1996 (Rel. 33, Created)  
DI 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE GAF2 PROTEIN (CAF-2).  
OS CAF2 OR SPAC23E2.01.  
GN Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hoe K.-L., Park S.-K., Yoo O.-J.J., Yoo H.-S.;  
RL Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972;  
CA Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;  
CL Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.  
CC -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).  
-----  
CC -!- SIMILARITY: BELONGS TO THE GATA-TYPE TRANSCRIPTION FACTOR FAMILY.  
-----  
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CC or send an email to license@isb-sib.ch).  
-----  
CC EMBL; L29051; AAB38022.1; -.  
DR EMBL; Z68887; CAAG3113.1; -.  
DR HSSP; P17429; 5CAT.  
DR InterPro; IPR000679; .  
DR Pfam; PF00320; GATA; 2.  
DR PRINTS; PR00619; GATAZNFINGER.  
DR PROSITE; PS00344; GATA_ZN_FINGER_1; 2.  
DR PROSITE; PS01114; GATA_ZN_FINGER_2; 2.  
RW Transcription regulation; DNA-binding; Zinc-finger; Nuclear protein.  
FT ZN_FING 12 36 GATA-TYPE (BY SIMILARITY).  
FT ZN_FING 172 196 GATA-TYPE (BY SIMILARITY).  
FT ZN_CONFLICT 182 182 L -> K (IN REF. 1).
```

SQ SEQUENCE 564 AA; 60611 MW; 0ED74CE0B6E210B7 CRC64;

Query Match 37.2%; Score 51; DB 1; Length 564;  
Best Local Similarity 47.6%; Pred. NO. 3.3;  
Matches 10; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

QY 5 IQLMHNLCGLKHLNMXRVLEWR 25  
||:||||:|:|:||||  
DB 519 IOELHNLNQHIOQID--EWLR 537

## RESULT 11

ID CDPK\_SOYBN STANDARD; PRT; 508 AA.  
AC P28583;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE CALCIUM-DEPENDENT PROTEIN KINASE SK5 (EC 2.7.1.-) (CDPK).  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;  
OC Fabales; Fabaceae; Papilionoideae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. WILLIAMS;  
RX MEDLINE=91240279; PubMed=1852075;  
RA Harper J.F., Sussman M.R., Schaller G.E., Putnam-Evans C.,  
RA Charbonneau H., Harmon A.C.;  
RT "A calcium-dependent protein kinase with a regulatory domain similar  
RT to calmodulin.";  
RL Science 252:951-954(1991).  
CC -!- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT  
CC INVOLVE CALCIUM AS A SECOND MESSENGER.  
CC -!- ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY  
CC PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.  
CC -!- TISSUE SPECIFICITY: FOUND THROUGHOUT THE PLANT.  
CC -!- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN SOYBEAN.  
CC -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-  
CC PROTEIN KINASES. BELONGS TO THE CAMK SUBFAMILY.  
CC -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.  
CC -----  
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EMBL; M64987; AB00806.1; -;  
DR PIR; A43713; A43713.  
DR HSSP; Q63450; 1A06.  
DR InterPro; IPR000719; -;  
DR InterPro; IPR002048; -;  
DR InterPro; IPR002290; -;  
DR Pfam; PF00036; ehand; 4;  
DR Pfam; PF00069; pkinase; 1.  
DR PROSITE; PS00018; EF\_HAND; 4.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
KW Calcium-binding; Phosphorylation.  
FT DOMAIN 34 292 PROTEIN KINASE.  
FT NP\_BIND 40 48 ATP (BY SIMILARITY).  
FT BINDING 63 63 ATP (BY SIMILARITY).  
FT ACT\_SITE 158 158 BY SIMILARITY.  
FT CA\_BIND 348 359 SITE 1 (POTENTIAL).  
FT CA\_BIND 384 395 SITE 2 (POTENTIAL).  
FT CA\_BIND 420 431 SITE 3 (POTENTIAL).

FT CA\_BIND 454 465 SITE 4 (POTENTIAL).  
SQ SEQUENCE 508 AA; 57169 MW; AFCDC51224192E4 CRC64;

Query Match 36.9%; Score 50.5; DB 1; Length 508;  
Best Local Similarity 52.6%; Pred. NO. 3.5;  
Matches 10; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

QY 4 ETQLMHNLCGLKHLNMXRYVE 22  
|||:||||:|:|:|:|  
DB 82 ETQIMHHLSEHAN-VVRIE 99

## RESULT 12

TORA\_ECOLI  
ID TORA\_ECOLI STANDARD; PRT; 848 AA.  
AC P33225; P78227;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE TRIMETHYLAMINE-N-OXIDE REDUCTASE PRECURSOR (EC 1.6.6.9) (TMAO  
DE REDUCTASE) (TRIMETHYLAMINE OXIDASE).  
GN TORA.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OX Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 40-46.  
RC STRAIN=K12;  
RX MEDLINE=94293785; PubMed=8022286;  
RA Mejean V., Lobbi-Nivol C., Lepelletier M., Giordano G., Chippaux M.,  
RA Pascal M.-C.;  
RT "TMAO anaerobic respiration in Escherichia coli: involvement of the  
RT tor operon.";  
RL Mol. Microbiol. 11:1169-1179(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=97061202; PubMed=8905232;  
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
RA Ikenoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,  
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
RA Yano M., Horiuchi T.;  
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome  
RT corresponding to the 12.7-28.0 min region on the linkage map.";  
RL DNA Res. 3:137-155(1996).  
RN [4]  
RP SEQUENCE OF 767-848 FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=94134696; PubMed=8302830;  
RA Ueguchi C., Kakeda M., Yamada H., Mizuno T.;  
RT "An analogue of the DnaJ molecular chaperone in Escherichia coli.";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:1054-1058(1994).  
CC -!- FUNCTION: REDUCES TRIMETHYLAMINE-N-OXIDE (TMAO) INFO  
CC TRIMETHYLAMINE; AN ANAEROBIC REACTION COUPLED TO ENERGY-YIELDING  
CC REACTIONS.  
CC -!- CATALYTIC ACTIVITY: NADH + TRIMETHYLAMINE-N-OXIDE = NAD(+) +  
CC TRIMETHYLAMINE + H(2)O.  
CC -!- SUBCELLULAR LOCATION: PERIPLASMIC.  
CC -!- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING

OXIDOREDUCTASE FAMILY.

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DR	EMBL; X73888; CAA52095.1; -.	
DR	EMBL; AF000201; AAC74082.1; -.	
DR	EMBL; D90736; BAA36139.1; -.	
DR	EMBL; D90737; BAA35764.1; -.	
DR	EMBL; D16500; -; NOT_ANNOTATED_CDS.	
DR	PIR; S34222; S34222.	
DR	HSP; Q57366; LCXT.	
DR	Ecogene; EG11814; torA.	
DR	InterPro; IPR001467; -.	
DR	Pfam; PF01568; Molybdop_binding; 1.	
DR	Pfam; PF00384; molybdopterin; 1.	
DR	PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; FALSE_NEG.	
DR	PROSITE; PS00490; MOLYBDOPTERIN_PROK_2; 1.	
DR	PROSITE; PS00932; MOLYBDOPTERIN_PROK_3; 1.	
KW	oxidoreductase; NAD; Molybdenum; Periplasmic; Signal.	
	SIGNAL	1 39
FT	CHAIN	40 848
FT	CONFLICT	173 173
FT	CONFLICT	176 176
FT	CONFLICT	256 256
FT	CONFLICT	258 258
FT	CONFLICT	281 281
FT	CONFLICT	325 325
FT	CONFLICT	348 348
FT	CONFLICT	503 504
FT	CONFLICT	713 714
FT	CONFLICT	751 751
FT	CONFLICT	781 781
FT	SEQUENCE	848 AA; 94455 MW; 59DDACB00B1843E7 CRC64;

Query Match	36.5%;	Score 50;	DB 1;	Length 848;
Best Local Similarity	45.0%;	Pred. No. 7;		
Matches 9;	Conservative 4;	Mismatches 7;	Indels 0;	Gaps 0;

QY 8 MHNLGKHLNSMXRVEWLKK 27  
: | | : | | | | | :  
Db 94 VHNAARIRYPMVRVDWLKR 113

```

RESULT 13
PGDR_MOUSE
ID PGDR_MOUSE STANDARD; PRT; 1098 AA.
AC P05622;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE BETA PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112)
DE (PDGF-R-BETA).
DE (PDGFR OR PDGFR.
OS Mus musculus (Mouse)).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RX [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP
RP TISSUE-Fibroblast;
RX MEDLINE=87014762; PubMed=3020426;
RA Yarden Y., Escobedo J.A., Kuang W.-J., Yang-Feng T.L., Daniel T.O.,
RA Tremble P.M., Chen E.Y., Ando M.E., Harkins R.N., Francke U.,
RA Fried V.A., Ullrich A., Williams L.T.;
RA "Structure of the receptor for platelet-derived growth factor helps
RT define a family of closely related growth factor receptors.";
RT

```

Nature 323:226-232(1986).

- 1- FUNCTION: THIS RECEPTOR BINDS PLATELET-DERIVED GROWTH FACTOR AND HAS A TYROSINE-PROTEIN KINASE ACTIVITY. THIS RECEPTOR BINDS SPECIFICALLY TO PDGF-B.
- 1- SUBUNIT: DIMER OF EITHER ALPHA-ALPHA, BETA-BETA OR ALPHA-BETA SUBUNITS.
- 1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
- 1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-PROTEIN KINASES.
- 1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE DOMAINS.

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DR	EMBL; X04367; CAA27892.1; -.
DR	PIR; A25742; PFMSRB.
DR	MGD; MGI:97531; Pdgfrb.
DR	InterPro; IPR000719; -.
DR	InterPro; IPR001245; -.
DR	InterPro; IPR001824; -.
DR	InterPro; IPR003006; -.
DR	Pfam; PF00047; ig; 4.
DR	Pfam; PF00069; pkinase; 2.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR	PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW	Tyrosine-protein kinase; Receptor; Transmembrane; Glycoprotein;
KW	Transferase; Phosphorylation; ATP-binding; Immunoglobulin domain;
KW	Signal.
FT	SIGNAL
FT	CHAIN
FT	32 1098
FT	BETA PLATELET-DERIVED GROWTH FACTOR RECEPTOR.
FT	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN
FT	32 530

330	FT	DOMAIN	IG-LIKE C2-TYPE DOMAIN.	(POTENTIAL).	
33	119	FT	IG-LIKE C2-TYPE DOMAIN.		
128	209	FT	IG-LIKE C2-TYPE DOMAIN.		
214	310	FT	IG-LIKE C2-TYPE DOMAIN.		
415	527	FT	IG-LIKE C2-TYPE DOMAIN.		
599	961	FT	PROTEIN KINASE.		
53	99	FT	POTENTIAL.		
148	189	FT	POTENTIAL.		
234	290	FT	POTENTIAL.		
435	507	FT	POTENTIAL.		
605	613	FT	ATP (BY SIMILARITY).		
633	633	FT	ATP (BY SIMILARITY).		
825	825	FT	BY SIMILARITY.		
750	750	FT	PHOSPHORYLATION (AUTO-)	(BY SIMILARITY).	
856	856	FT	PHOSPHORYLATION (AUTO-)	(BY SIMILARITY).	
44	44	FT	N-LINKED (GLCNAC. .)	(POTENTIAL).	
88	88	FT	N-LINKED (GLCNAC. .)	(POTENTIAL).	
102	102	FT	N-LINKED (GLCNAC. .)	(POTENTIAL).	
214	214	FT	N-LINKED (GLCNAC. .)	(POTENTIAL).	
291	291	FT	N-LINKED (GLCNAC. .)	(POTENTIAL).	
306	306	FT	N-LINKED (GLCNAC. .)	(POTENTIAL).	
353	353	FT	N-LINKED (GLCNAC. .)	(POTENTIAL).	
370	370	FT	N-LINKED (GLCNAC. .)	(POTENTIAL).	
444	444	FT	N-LINKED (GLCNAC. .)	(POTENTIAL).	
467	467	FT	N-LINKED (GLCNAC. .)	(POTENTIAL).	
478	478	FT	N-LINKED (GLCNAC. .)	(POTENTIAL).	
1098	AA: 122805	MM: 8D39131	CAFCAC3FC31D	CRC64:	
SEQUENCE					

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Query Match      34.3%; Score 47; DB 1; Length 1098;
Best Local Similarity 53.3%; Pred. No. 26;
Matches      8; Conservative      5; Mismatches      2; Indels      0; Gaps      0;
```





```
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91065532; PubMed-2249778;
RA Mangin M., Ikeda K., Broadus A.E.;
RT "Structure of the mouse gene encoding parathyroid hormone-related
RT peptide."
RL Gene 95:195-202(1990).
CC -!- FUNCTION: PLAYS A PHYSIOLOGICAL ROLE IN LACTATION, POSSIBLY AS A
CC HORMONE FOR THE MOBILIZATION AND/OR TRANSFER OF CALCIUM TO THE
CC MILK.
CC -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M60057; AAA63639.1;
DR EMBL; M60058; AAA63639.1; JOINED.
DR EMBL; M60056; AAA63639.1; JOINED.
DR PIR; JN0103; JN0103.
DR MGD; MGI:97800; Pchlh.
DR InterPro; IPR001415;
DR Pfam; PF01279; Parathyroid; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Calcium; Hormone; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT PROPEP 25 36
FT CHAIN 37 175 PARATHYROID HORMONE-RELATED PROTEIN.
SQ SEQUENCE 175 AA; 20100 MW; 6D27CFCC31900B45 CRC64;
```

```
Query Match 33.6%; Score 46; DB 1; Length 175;
Best Local Similarity 47.4%; Pred. NO. 5.5;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 VSEIQLMHNIGKHLNSMXR 20
DB 38 VSEHQLLDKGRSIQDLRR 56
```

Search completed: August 31, 2001, 16:01:46  
Job time: 110 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 31, 2001, 15:59:56 ; Search time 12.82 Seconds  
(without alignments)  
166.372 Million cell updates/sec

Title: US-09-448-867-1  
Perfect score: 137  
Sequence: 1 XYSEIQMHNGLKHLNMXRVEWLKKL 28  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	134	97.8	115	1 PTHU	parathyroid hormon
2	126	92.0	115	1 PTGP	parathyroid hormon
3	125	91.2	115	1 PTBO	parathyroid hormon
4	125	91.2	115	2 JC4202	parathyroid hormon
5	116	84.7	115	2 A05091	parathyroid hormon
6	115	83.9	105	2 I51851	parathyroid hormon
7	90	65.7	119	2 A34937	parathyroid hormon
8	54	39.4	824	2 F72408	leucine-tRNA liga
9	52	38.0	363	2 F70195	UDP-N-acetylglucos
10	51	37.2	564	2 T38291	GATA-type transcri
11	51	37.2	564	2 T32998	transcription fact
12	50.5	36.9	508	1 A43713	calcium-dependent
13	50	36.5	336	2 F84056	hypothetical prote
14	50	36.5	848	2 C64841	trimethylamine-N-o
15	50	36.5	848	2 D85635	trimethylamine N-o
16	49	35.8	115	2 H72705	hypothetical prote
17	47	34.3	207	2 A64655	hypothetical prote
18	47	34.3	256	2 T25913	hypothetical prote
19	47	34.3	339	2 T18926	hypothetical prote
20	47	34.3	1048	2 T30815	platelet-derived g
21	47	34.3	1098	1 PFMSRB	platelet-derived g
22	47	34.3	1106	1 PFHUGB	platelet-derived g
23	46.5	33.9	544	2 T17422	halogenase-like pr
24	46	33.6	175	1 JN0103	parathyroid hormon
25	46	33.6	176	1 T51020	parathyroid hormon
26	46	33.6	177	1 PTHU2L	parathyroid hormon
27	46	33.6	177	1 A30012	parathyroid hormon
28	46	33.6	177	2 JC4201	parathyroid hormon
29	46	33.6	183	1 FRRTL	ferritin light cha

30	46	33.6	209	1 PTHU3L	parathyroid hormon
31	46	33.6	211	2 S43133	hypothetical prote
32	46	33.6	297	2 F82039	ribonuclease BN VC
33	46	33.6	323	2 F84423	hypothetical prote
34	46	33.6	457	2 S44269	platelet-derived g
35	46	33.6	490	2 T08873	calcium-dependent
36	46	33.6	495	1 S46284	calcium-dependent
37	46	33.6	501	2 G85097	hypothetical prote
38	46	33.6	538	2 E64563	ctp synthetase - H
39	46	33.6	538	2 C71946	ctp synthetase - Hel
40	46	33.6	1087	2 I51552	platelet-derived g
41	46	33.6	1088	1 PFRTGA	platelet-derived g
42	46	33.6	1089	1 PFHUGA	platelet-derived g
43	46	33.6	1089	1 S33727	platelet-derived g
44	45.5	33.2	528	2 D65214	hypothetical 60.8
45	45.5	33.2	528	2 G86099	hypothetical prote

## ALIGNMENTS

RESULT 1

PTHU

parathyroid hormone precursor [validated] - human

N;Alternate names: parathyroid hormone

C;Species: Homo sapiens (man)

C;Date: 24-Apr-1984 #sequence\_revision 19-Jan-1996 #text\_change 08-Dec-2000

C;Accession: A19339; S53790; A93169; S21199; A93789; A93783; A90426; A94410;

R;Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr.

Proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983

A;Title: Nucleotide sequence of the human parathyroid hormone gene.

A;Reference number: A19339; MUID:83169834

A;Accession: A19339

A;Molecule type: DNA

A;Residues: 1-115 <VAS>

A;Cross-references: GB:J00301; NID:g190702; PIDN:AAA60215.1; PID:g190704

R;Yamauchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K.

Biol. Chem. Hoppe-Seyler 375, 821-824, 1994

A;Title: Purification of meprin from human kidney and its role in parathyroid hormone

A;Reference number: S53790; MUID:95225988

A;Accession: S53790

A;Molecule type: protein

A;Residues: 'X',33,'X',35-46;65-84;105-110 <AM>

A;Note: peptides generated in vitro and in vivo by meprin; peptide cleavage also occu

R;Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.

Nature 249, 155-157, 1974

A;Title: Structural analysis of human parathyroid hormone by a new microsequencing

A;Reference number: A93169; MUID:74174967

A;Accession: A93169

A;Molecule type: protein

A;Residues: 26-37 <JAC>

R;Olstad, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gautvik,

Eur. J. Biochem. 205, 311-319, 1992

A;Title: Isolation and characterization of two biologically active O-glycosylated for

ation.

A;Reference number: S21199; MUID:92209518

A;Accession: S21199

A;Molecule type: protein

A;Residues: 32-114,'N' <OLS>

A;Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosylati

R;Niall, H.D.; Sauer, R.T.; Jacobs, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan, J.L

Proc. Natl. Acad. Sci. U.S.A. 71, 384-388, 1974

A;Title: The amino-acid sequence of the amino-terminal 37 residues of human parathyro

A;Reference number: A93789; MUID:74111656

A;Accession: A93789

A;Molecule type: protein

A;Residues: 32-68 <NIA>

R;Brewer Jr., H.B.; Fairwell, T.; Ronan, R.; Sizemore, G.W.; Arnaud, C.D.

Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972

A;Title: Human parathyroid hormone: amino-acid sequence of the amino-terminal residue

A;Reference number: A93783; MUID:73070429

A;Accession: A93783

A;Molecule type: protein

A:Residues: 32-52,'Q',54-58,'K',60,'L',62-65 <BRE>  
 A:Note: This sequence was determined by sequenator and mass spectroscopic identification  
 R:Keutmann, H.T.; Niall, H.D.; O'Riordan, J.L.H.; Potts Jr., J.T.  
 Biochemistry 14, 1842-1847, 1975  
 A:Title: A reinvestigation of the amino-terminal sequence of human parathyroid hormone.  
 A:Reference number: A90387; MUID:75146516  
 A:Accession: A90387  
 A:Molecule type: protein  
 A:Residues: 52-75 <KE3>  
 R:Keutmann, H.T.; Sauer, M.M.; Hendy, G.N.; O'Riordan, J.L.H.; Potts Jr., J.T.  
 Biochemistry 17, 5723-5729, 1978  
 A:Title: Complete amino acid sequence of human parathyroid hormone.  
 A:Reference number: A90426; MUID:79082855  
 A:Accession: A90426  
 A:Molecule type: protein  
 A:Residues: 61-106,'D',108-115 <KEU>  
 R:Keutmann, H.T.; Niall, H.D.; Jacobs, J.W.; Barling, P.M.; Hendy, G.N.; O'Riordan, J.L.H.  
 in Calcium-regulating Hormones, Talmadge, R.V., Owen, M., and Parsons, J.A., eds., pp.9-  
 A:Reference number: A94410  
 A:Accession: A94410  
 A:Molecule type: protein  
 A:Residues: 75-100 <KE2>  
 R:Tregear, G.W.; van Rietschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parsons, J.  
 Hoppe-Seyler's Z. Physiol. Chem. 355, 415-421, 1974  
 A:Title: Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of human  
 A:Reference number: A91660; MUID:75059220  
 A:Contents: annotation; synthesis of residues 32-65  
 A:Note: the biologically active amino-terminal 34 residues of parathyroid hormone were  
 at renal adenylate cyclase assay and with the bovine hormone's active region in the child  
 R:Andreatta, R.H.; Hartmann, A.; Joehl, A.; Kamber, B.; Maier, R.; Riniker, B.; Rittel,  
 Helv. Chim. Acta 56, 470-473, 1973  
 A:Title: Synthese der Sequenz 1-34 von menschlichem Parat-hormon.  
 A:Reference number: A91635; MUID:73227467  
 A:Contents: annotation; synthesis of residues 32-65  
 A:Note: the amino-terminal 34 residues of the parathyroid hormone sequence as determined  
 into thyroparathyroidectomized rats caused a distinct increase in plasma calcium level  
 R:Hendy, G.N.; Kronenberg, H.M.; Potts, J.T.  
 Proc. Natl. Acad. Sci. U.S.A. 78, 7365-7369, 1981  
 A:Title: Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.  
 A:Reference number: I38342; MUID:82150870  
 A:Accession: I38342  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-115 <RES>  
 A:Cross-references: EMBL:Y00597; NID:g37143; PIDN:CAA23843.1; PID:g37144  
 C:Genetics:  
 A:Gene: GDB:PTH  
 A:Cross-references: GDB:l119522; OMIM:168450  
 A:Map position: 11p15.2-11p15.1  
 A:Introns: 29/2  
 A:Note: the first intron occurs before the initiator codon  
 C:Function:  
 A:Description: factor in homeostatic control of plasma calcium and phosphate; released b  
 counter to calcitonin  
 C:Superfamily: parathyroid hormone; parathyroid hormone homology  
 C:Keywords: calcium; hormone; parathyroid gland; plasma  
 F:1-25/Domain: signal sequence #status predicted <SIG>  
 F:26-31/Domain: propeptide #status experimental <PRO>  
 F:30-64/Domain: parathyroid hormone homology <PTH>  
 F:32-115/Product: parathyroid hormone #status experimental <MAT>

Query Match 97.8%; Score 134; DB 1; Length 115;  
 Best Local Similarity 96.3%; Pred. No. 7.1e-13;  
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMXRVLEWLRKKL 28  
 |||||  
 Db 33 VSEIQLMHNLGKHLNSMXRVLEWLRKKL 59

RESULT 2  
 PTPG

parathyroid hormone precursor - pig  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 24-Apr-1984 #sequence.revision 12-Apr-1996 #text\_change 18-Jun-1999  
 C:Accession: B26806; A90390; A90376; A01535  
 R:Schmelzer, H.J.; Gross, G.; Wildera, G.; Mayer, H.  
 Nucleic Acids Res. 15, 6740, 1987  
 A:Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid h  
 A:Reference number: A26806; MUID:87316938  
 A:Accession: B26806  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-115 <SCH>  
 A:Cross-references: GB:X05722; GB:Y00409; NID:gl838; PIDN:CAA29193.1; PID:gl839  
 R:Chu, L.L.H.; Huang, W.Y.; Littledike, E.T.; Hamilton, J.W.; Cohn, D.V.  
 Biochemistry 14, 3631-3635, 1975  
 A:Title: Porcine preproparathyroid hormone. Identification, biosynthesis, and partial am  
 A:Reference number: A90390; MUID:76018954  
 A:Accession: A90390  
 A:Molecule type: protein  
 A:Residues: 26-115 <CHU>  
 R:Sauer, R.T.; Niall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts Jr.  
 Biochemistry 13, 1994-1999, 1974  
 A:Title: The amino acid sequence of porcine parathyroid hormone.  
 A:Reference number: A90376; MUID:74253317  
 A:Accession: A90376  
 A:Molecule type: protein  
 A:Residues: 32-109 <SAU>  
 R:Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.  
 Am. J. Med. 56, 759-766, 1974  
 A:Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hor  
 A:Reference number: A90030; MUID:74173303  
 A:Contents: annotation  
 C:Superfamily: parathyroid hormone; parathyroid hormone homology  
 C:Keywords: calcium; hormone; parathyroid gland  
 F:1-25/Domain: signal sequence #status predicted <SIG>  
 F:26-31/Domain: propeptide #status experimental <PRO>  
 F:30-64/Domain: parathyroid hormone homology <PTH>  
 F:32-115/Product: parathyroid hormone #status experimental <MAT>  
 Query Match 92.0%; Score 126; DB 1; Length 115;  
 Best Local Similarity 88.9%; Pred. No. 1.1e-11;  
 Matches 24; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 VSEIQLMHNLGKHLNSMXRVLEWLRKKL 28  
 |||||  
 Db 33 VSEIQLMHNLGKHLNSMXRVLEWLRKKL 59  
 RESULT 3  
 PTPG  
 parathyroid hormone precursor - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 23-Oct-1981 #sequence.revision 23-Oct-1981 #text\_change 18-Jun-1999  
 C:Accession: A24949; A93835; A93793; A91648; A93773; I45975; I45976; A01534  
 R:Weaver, C.A.; Gordon, D.F.; Kissil, M.S.; Mead, D.A.; Kemper, B.  
 Gene 28, 319-329, 1984  
 A:Title: Isolation and complete nucleotide sequence of the gene for bovine parathyroi  
 A:Reference number: A24949; MUID:84262483  
 A:Accession: A24949  
 A:Molecule type: DNA  
 A:Residues: 1-115 <WEA>  
 A:Cross-references: GB:K01938  
 R:Kronenberg, H.M.; McDevitt, B.E.; Majzoub, J.A.; Nathans, J.; Sharp, P.A.; Potts Jr  
 Proc. Natl. Acad. Sci. U.S.A. 76, 4981-4985, 1979  
 A:Title: Cloning and nucleotide sequence of DNA coding for bovine preproparathyroid h  
 A:Reference number: A93835; MUID:80056617  
 A:Accession: A93835  
 A:Molecule type: DNA  
 A:Residues: 1-115 <KRO>  
 A:Cross-references: GB:Y00106; GB:J00023; NID:g84; PIDN:CAA23439.1; PID:g85  
 A:Note: the authors translated the codon GAA for residue 50 as Gly  
 R:Hamilton, J.W.; Niall, H.D.; Jacobs, J.W.; Keutmann, H.T.; Potts Jr., J.T.; Cohn, D

Proc. Natl. Acad. Sci. U.S.A. 71, 653-656, 1974  
A:Title: The N-terminal amino-acid sequence of bovine parathyroid hormone.  
A:Reference number: A93793; MUID:74142666  
A:Accession: A93793  
A:Molecule type: protein  
A:Residues: 26-115 <HAM>  
R:Niall, H.D.; Keutmann, H.T.; Sauer, R.; Hogan, M.L.; Dawson, B.F.; Aurbach, G.D.; Potts  
Hoppe-Seyler's Z. Physiol. Chem. 351, 1586-1588, 1970  
A:Title: The amino acid sequence of bovine parathyroid hormone I.  
A:Reference number: A91648; MUID:71076162  
A:Accession: A91648  
A:Molecule type: protein  
A:Residues: 32-115 <NIA>  
R:Brewer Jr., H.B.; Ronan, R.  
Proc. Natl. Acad. Sci. U.S.A. 67, 1862-1869, 1970  
A:Title: Bovine parathyroid hormone: amino acid sequence.  
A:Reference number: A93773; MUID:71063634  
A:Accession: A93773  
A:Molecule type: protein  
A:Residues: 32-115 <BRE>  
R:Potts Jr., J.T.; Tregear, G.W.; Keutmann, H.T.; Niall, H.D.; Sauer, R.; Deftos, L.J.;  
Proc. Natl. Acad. Sci. U.S.A. 68, 63-67, 1971  
A:Title: Synthesis of a biologically active N-terminal tetraoctapeptide of parathyroid hormone.  
A:Reference number: A93776; MUID:71091588  
A:Contents: annotation; synthesis of residues 32-65  
A:Note: the synthetic peptide was active in vivo and in vitro  
R:Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.  
Am. J. Med. 56, 759-766, 1974  
A:Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone  
A:Reference number: A90030; MUID:74173303  
A:Contents: annotation  
R:Weaver, C.A.; Gordon, D.F.  
Proc. Natl. Acad. Sci. U.S.A. 78, 4073-4077, 1981  
A:Title: Introduction by molecular cloning of artifactual inverted sequences at the 5' terminus of the parathyroid hormone gene.  
A:Reference number: 145975; MUID:82037785  
A:Accession: 145975  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-115 <WE2>  
A:Cross-references: GB:J00024; NID:g163642; PIDN:AAA30747.1; PID:g163643  
R:Weaver, C.A.; Gordon, D.F.  
Mol. Cell. Endocrinol. 28, 411-424, 1982  
A:Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA.  
A:Reference number: 145976; MUID:83105964  
A:Accession: 145976  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-115 <WE3>  
A:Cross-references: GB:M25082; NID:g163644; PIDN:AAA30748.1; PID:g163645  
C:Genetics:  
A:Gene: PTH  
A:Introns: 29/2  
C:Superfamily: parathyroid hormone; parathyroid hormone homology  
C:Keywords: hormone  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-115/Product: parathyroid hormone #status experimental <PMAT>  
F:26-31/Domain: propeptide #status experimental <PRO>  
F:30-64/Domain: parathyroid hormone homology <PTH>  
F:32-115/Product: parathyroid hormone #status experimental <MAT>

Query Match 91.2%; Score 125; DB 1; Length 115;  
Best Local Similarity 88.9%; Pred. No. 1.5e-11;  
Matches 24; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMXRVEWLRKKL 28  
||||| ||||||| ||| |||||||  
Db 33 VSEIQFMHNLGKHLSSMERVWLRKKL 59

RESULT 4  
JCA202  
parathyroid hormone precursor - dog

C:Species: Canis lupus familiaris (dog)  
C:Date: 10-Sep-1995 #sequence\_revision 27-Oct-1995 #text\_change 16-Jul-1999  
C:Accession: JCA202  
R:Rosol, T.J.; Steinmeyer, C.L.; McCauley, L.K.; Groene, A.; DeWille, J.W.; Capen, C.  
Gene 160, 241-243, 1995  
A:Title: Sequences of the cDNAs encoding canine parathyroid hormone-related protein a  
A:Reference number: JCA201; MUID:95369696  
A:Accession: JCA202  
A:Molecule type: mRNA  
A:Residues: 1-115 <ROS>  
A:Cross-references: GB:U15662; NID:g558915; PIDN:AAA82584.1; PID:g558916  
C:Superfamily: parathyroid hormone; parathyroid hormone homology  
C:Keywords: hormone  
F:1-31/Domain: signal sequence #status predicted <SIG>  
F:30-64/Domain: parathyroid hormone homology <PTH>  
F:32-115/Product: parathyroid hormone #status predicted <MAT>

Query Match 84.7%; Score 116; DB 2; Length 115;  
Best Local Similarity 81.5%; Pred. No. 3.4e-10;  
Matches 22; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMXRVEWLRKKL 28  
||||| ||||||| ||| |||||||  
Db 33 VSEIQLMHNLGKHLASVERQWLRKKL 59

RESULT 6  
I51851  
parathyroid hormone - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 16-Jul-1999  
C:Accession: I51851  
R:Schmelzer, H.  
Adv. Gene Technol. 21, 228-229, 1984

A;Title: Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone.

A;Reference number: I51851  
 A;Accession: I51851  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-105 <RES>  
 A;Cross-references: GB:M54875; NID:g601932; PIDN:AAA57156.1; PID:g601933  
 C;Genetics:  
 C;Superfamily: parathyroid hormone; parathyroid hormone homology  
 F;20-54/Domain: parathyroid hormone homology <PTH>

Query Match 83.9%; Score 115; DB 2; Length 105;  
 Best Local Similarity 77.8%; Pred. No. 4.3e-10;  
 Matches 21; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMXRVEWLRKKL 28  
 DB 23 ISEIQLMHNLGKHLASVERMQLRKKL 49

RESULT 7

A34937  
 parathyroid hormone precursor - chicken  
 C;Species: Gallus gallus (chicken)  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 16-Jul-1999  
 C;Accession: A34937; I50411  
 R;Russell, J.; Sherwood, L.M.  
 Mol. Endocrinol. 3, 325-331, 1989  
 A;Title: Nucleotide sequence of the DNA complementary to avian (chicken) preproparathyroid hormone  
 A;Reference number: A34937; MUID:89219100  
 A;Accession: A34937  
 A;Molecule type: mRNA  
 A;Residues: 1-119 <RUS>  
 A;Cross-references: GB:M31604; NID:g212767; PIDN:AAA49093.1; PID:g212768  
 R;Khosla, S.; Denay, M.; Pines, M.; Hurwitz, S.; Potts, J.T.  
 J. Bone Miner. Res. 3, 689-698, 1988  
 A;Title: Nucleotide sequence of cloned cDNAs encoding chicken preproparathyroid hormone.  
 A;Reference number: I50411; MUID:89284968  
 A;Accession: I50411  
 A;Status: preliminary; translated from GB/EMBL/DBJ

A;Residues: 1-119 <RHO>  
 A;Cross-references: GB:M36522; NID:g212591; PIDN:AAB02866.1; PID:g212592  
 C;Superfamily: parathyroid hormone; parathyroid hormone homology  
 F;1-25/Domain: signal sequence #status predicted <SIG>  
 F;26-31/Domain: propeptide #status predicted <PRO>  
 F;30-64/Domain: parathyroid hormone homology <PTH>  
 F;32-119/Product: parathyroid hormone #status predicted <MAT>

Query Match 65.7%; Score 90; DB 2; Length 119;  
 Best Local Similarity 59.3%; Pred. No. 2.6e-06;  
 Matches 16; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMXRVEWLRKKL 28  
 DB 33 VSEQLMHNLGHEHRTVERDQLQMKL 59

RESULT 8

F72408  
 leucine--tRNA ligase (EC 6.1.1.4) - Thermotoga maritima (strain MSB8)  
 C;Species: Thermotoga maritima  
 C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
 C;Accession: F72408  
 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.  
 Nature 399, 323-329, 1999  
 A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing  
 A;Reference number: A72200; MUID:99287316

A;Accession: F72408  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-824 <ARN>  
 A;Cross-references: GB:AE001702; GB:AE000512; NID:g4980662; PIDN:AAD35261.1; PID:g498  
 A;Experimental source: strain MSB8  
 C;Genetics:  
 A;Gene: TM0168  
 C;Superfamily: leucine--tRNA ligase  
 C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 39.4%; Score 54; DB 2; Length 824;  
 Best Local Similarity 41.7%; Pred. No. 4.7;  
 Matches 10; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 5 IOLMHNLGKHLNSMXRVEWLRKKL 28  
 DB 692 MELVNHLSQYLNVPQEEWNRKLL 715

RESULT 9

F70195  
 UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N  
 C;Species: Borrelia burgdorferi (Lyme disease spirochete)  
 C;Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 24-Nov-1999  
 C;Accession: F70195  
 R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh  
 son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vu  
 ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.  
 Nature 390, 580-586, 1997  
 A;Authors: Smith, H.O.; Venter, J.C.  
 A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.  
 A;Reference number: A70100; MUID:98065943  
 A;Accession: F70195  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-363 <KLE>  
 A;Cross-references: GB:AE001176; GB:AE000783; NID:g2688699; PIDN:AAC67113.1; PID:g268  
 A;Experimental source: strain B31  
 C;Superfamily: murG protein

Query Match 38.0%; Score 52; DB 2; Length 363;  
 Best Local Similarity 36.0%; Pred. No. 3.9;  
 Matches 9; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 3 SEIQLMHNLGKHLNSMXRVEWLRKK 27  
 DB 217 AEIVFIHQSGKNLNDLSEKNYLRQ 241

RESULT 10

T38291  
 GATA-type transcription factor family protein Gaf2p - fission yeast (Schizosaccharomy  
 C;Species: Schizosaccharomyces pombe  
 C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
 C;Accession: T38291  
 R;Skeltton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.  
 submitted to the EMBL Data Library, January 1996  
 A;Reference number: Z21784  
 A;Accession: T38291  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-564 <SRE>  
 A;Cross-references: EMBL:Z68887; PIDN:CAA93113.1; GSPDB:GN000066; SPDB:SPAC23E2.01  
 A;Experimental source: strain 972h.; cosmid c23E2  
 C;Genetics:  
 A;Gene: SPDB:SPAC23E2.01  
 A;Map position: 1

Query Match 37.2%; Score 51; DB 2; Length 564;

Best Local Similarity 47.6%; Pred. No. 8.8;  
Matches 10; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

Qy 5 IQLMHNIGKHLNSMXRVEWLR 25  
II : III : I : IIII  
Db 519 IQELHNLNQHIQQID--EWLR 537

RESULT 11  
T43298  
transcription factor gaf2 - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T43298  
R:Ho, K.L.; Won, M.S.; Yoo, O.J.; Yoo, H.S.  
Biochem. Mol. Biol. Int. 39, 127-135, 1996  
A:Title: Molecular cloning of GAR2, a Schizosaccharomyces pombe GATA factor, which has  
A:Reference number: 222402; MUID:96392547  
A:Accession: T43298  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-564 <HOE>  
A:Cross-references: EMBL:L29051; NID:g703467; PIDN:AAB38022.1; PID:g703468  
C:Genetics:  
A:Gene: gaf2  
C:Keywords: transcription factor; transcription regulation; zinc finger

Query Match 37.2%; Score 51; DB 2; Length 564;  
Best Local Similarity 47.6%; Pred. No. 8.8;  
Matches 10; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

Qy 5 IQLMHNIGKHLNSMXRVEWLR 25  
II : III : I : IIII  
Db 519 IQELHNLNQHIQQID--EWLR 537

RESULT 12  
A43713  
calcium-dependent protein kinase (EC 2.7.1.-) - soybean  
C:Species: Glycine max (soybean)  
C:Date: 03-Mar-1993 #sequence\_revision 14-Jul-1994 #text\_change 11-Jun-1999  
C:Accession: A43713  
R:Harper, J.F.; Sussman, M.R.; Schaller, G.E.; Putnam-Evans, C.; Charbonneau, H.; Harmon  
Science 252, 951-954, 1991  
A:Title: A calcium-dependent protein kinase with a regulatory domain similar to calmodulin  
A:Reference number: A43713; MUID:91240279  
A:Accession: A43713  
A:Molecule type: mRNA  
A:Residues: 1-508 <HAR>  
A:Cross-references: EMBL:M64987; NID:g169930; PIDN:AAB00806.1; PID:g169931  
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin  
C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific  
F:32-292/Domain: protein kinase homology <KIN>  
F:40-48/Region: protein kinase ATP-binding motif  
F:335-367/Domain: calmodulin repeat homology <EF1>  
F:371-403/Domain: calmodulin repeat homology <EF2>  
F:407-439/Domain: calmodulin repeat homology <EF3>  
F:441-473/Domain: calmodulin repeat homology <EF4>  
F:63/Active site: Lys #status predicted

Query Match 36.9%; Score 50.5; DB 1; Length 508;  
Best Local Similarity 52.6%; Pred. No. 9.4;  
Matches 10; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

Qy 4 ETQLMHNIGKHLNSMXRVE 22  
II : III : I : I : I : I  
Db 82 ETQIMHHLSEHAN-VVRIE 99

RESULT 13  
F84056

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RESULT 15
D85635
trimethylamine N-oxide reductase subunit [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: D85635
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: D85635
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-848 <STO>
A:Cross-references: GB:AE005174; NID:g12514264; PIDN:AAG55544.1; GSPDB:GN00145; UWGP:Z14
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: torA
C:Superfamily: trimethylamine-N-oxide reductase

Query Match 36.5%; Score 50; DB 2; Length 848;
Best Local Similarity 45.0%; Pred. No. 19;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 8 MHNLGKHLNSMKRVEWLKK 27
   :|| : ||:||||
Db 94 VHNARIRYPMVRVDWLKR 113

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Search completed: August 31, 2001, 16:01:01  
Job time: 65 sec